

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:05:24 : Search time 4686 Seconds
(without alignment)
10423.145 Million cell updates/sec

Title: US-10-019-337e-7

Perfect score: 1008
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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hhg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sv: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	1008	6 AX068325	AX068325 Sequence
2	1008	100.0	1008	10 RNO294476	AJ294476 Rattus no
3	872	86.5	953	6 AX068324	AX068324 Sequence
4	872	86.5	953	10 RNO294475	AJ294475 Rattus no
5	666.2	66.1	909	10 MMU276516	AJ276516 Mus muscu
6	630.6	62.6	882	10 MMU276871	AJ276871 Mus muscu
7	593.8	58.7	834	10 MMU276514	AJ276514 Mus muscu
8	591.8	58.7	834	6 AX090389	AX090389 Sequence
9	558.2	55.4	783	6 AX090395	AX090395 Sequence
10	558.2	55.4	783	10 MMU276870	AJ276870 Mus muscu
11	510.6	50.7	795	6 AX090391	AX090391 Sequence
12	454.4	45.1	2522	6 AX068323	AX068323 Sequence
13	454.4	45.1	245589	2 AC094932	AC094932 Rattus no
14	430.6	42.7	1427	9 AP253318	AP253318 Homo sapi
15	427.6	42.4	810	9 HSA291673	AJ291673 Homo sapi
16	427.4	42.4	849	6 AX090393	AX090393 Sequence
17	356.8	35.4	15914	6 AX090388	AX090388 Sequence
18	356.8	35.4	47887	10 AP155960	AP155960 Mus muscu
19	356.8	35.4	189283	10 AL833771	AL833771 Mouse DNA

20	356.8	35.4	223026	2 AF415225	AF415225 Mus muscu
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22	330.8	31.8	900	9 HSA291674	AJ291674 Homo sapi
23	316.8	31.4	573	10 MMU276872	AJ276872 Mus muscu
24	291.4	28.9	549	9 HSA291675	AJ291675 Homo sapi
25	284	28.2	901	6 AX068321	AX068321 Sequence
26	258.8	25.7	792	6 AX068319	AX068319 Sequence
27	258.8	25.7	1792	10 AB041809	AB041809 Mus muscu
28	216.4	21.5	23379	9 AL356755	AL356755 Human DNA
29	216.4	21.5	206647	9 AP002898	AP002898 Homo sapi
30	216.4	21.5	207433	6 AX326809	AX326809 Sequence
31	209	20.7	872	6 AX068322	AX068322 Sequence
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33	208.6	20.7	167357	2 AC055771	AC055771 Homo sapi
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35	202	20.0	497	6 AX068320	AX068320 Sequence
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37	178.2	17.7	459	6 CQ728170	CQ728170 Sequence
38	151.4	15.0	966	9 AY326396	AY326396 Homo sapi
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ALIGNMENTS

RESULT 1
AX068325
LOCUS AX068325
DEFINITION Sequence 7 from Patent WO0102557.
ACCESSION AX068325
VERSION AX068325.1 GI:12578508

KEYWORDS

ORGANISM Rattus rattus (black rat)

REFERENCE

1 Maure, S.L., Clk, M. and Hoefnagel, E.W.
Neurotrophic factor receptor gfr-alpha-4
Patent: WO 0102557-A 7 11-JAN-2001;

JOURNAL

JANSEN PHARMACEUTICA N.V. (BE)

FEATURES

location/Qualifiers

SOURCE

1. 1008
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/mol_type="unassigned DNA"
/db_xref="taxon:10117"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7, 4e-161;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION Rattus norvegicus mRNA for neurotrophic factor receptor splice
          Variant B (Gfra4 gene).
ACCESSION AJ294476
VERSION   AJ294476.1
KEYWORDS  alternative splicing; Gfra4 gene; neurotrophic factor receptor;
          polymorphism; soluble isoform; variant B.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
          Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1
AUTHORS  Maure, S., Cik, M., Hofnagel, E., Noerat, C.A., Van der Linden, I.,
          Scott, R., Van Gompel, P., Lesage, A.S.J., Verhasselt, P., Ibanez, C.F.,
          and Gordon, R.D.

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TITLE   Mammalian GFRA4-4, a divergent member of the GFRA4 family of
JOURNAL coreceptors for glial cell line-derived neurotrophic factor family
MEDLINE ligands, is a receptor for the neurotrophic factor persephin
PUBMED  J. Biol. Chem. 275 (50), 39427-39434 (2000)
REFERENCE 10958791
AUTHORS 2 (bases 1 to 1008)
TITLE   Maure, S.L.
JOURNAL Direct Submission
        Submitted (01-SEP-2000) Maure S.L., Biotechnology &
        High-Throughput Screening, Janssen Research Foundation,
        Turnhoutseweg 30, B-2340 Beerse, BELGIUM
        Related splice variant: AJ294475.
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Best Local Similarity 100.0%; Pred. No. 7,4e-161;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTGTAAGCTTTAAGCAGAGAGACCTAAGACTGACATGCTATGTTAGTGAAGCG 60
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ACCESSION AJ294475
VERSION AJ294475.1
KEYWORDS GI:11191814
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1
AUTHORS Masure, S., Clik, M., Hofnagel, E., Noer, C.A., Van der Linden, I., Scott, R., Van Gompel, P., Leesge, A.S.J., Verhasselt, P., Ibanez, C.F., and Gordon, R.D.
TITLE Mammalian GFRalpha-4, a divergent member of the GFRalpha family of coreceptors for glial cell line-derived neurotrophic factor family 1 ligands, is a receptor for the neurotrophic factor persephin
JOURNAL J. Biol. Chem. 275 (50), 39427-39434 (2000)
MEDLINE 20564314
PUBMED 10958791
REFERENCE 2 (bases 1 to 953)
AUTHORS Masure, S.L.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2000) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse, BELGIUM
COMMENT Related splice variant: AJ294476.
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Best Local Similarity 93.6%; Pred. No. 7.5e-138;
Matches 943; Conservative 0; Mismatches 10; Indels 55; Gaps 1;
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RESULT 5
MMU276516 909 bp mRNA linear ROD 02-FEB-2001
LOCUS MMU276516
DEFINITION Mus musculus mRNA for putative GDNF family receptor alpha 4,
transmembrane isoform (Gfra4 gene).
ACCESSION AJ276516
VERSION AJ276516.1
KEYWORDS GDNF family receptor alpha 4; Gfra4 gene; transmembrane isoform.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Lindahl, M., Timmusk, T., Rossi, J., Saarna, M. and Airaksinen, M.S.
TITLE Expression and alternative splicing of mouse Gfra4 suggest roles in endocrine cell development
JOURNAL Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
MEDLINE 20319126
PUBMED 10860579

REFERENCE 2 (bases 1 to 909)
AUTHORS Airaksinen, M.S.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari 9), 00014 University of Helsinki, FINLAND

FEATURES
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ORIGIN
Query Match 66.1%; Score 666.2; DB 10; Length 909;
Best Local Similarity 86.3%; Pred. No. 4.9e-103;
Matches 781; Conservative 0; Mismatches 98; Indels 26; Gaps 3;

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QY 186 CGAGCAATGCCAGAGCTGCGCTCCAGTACGTGCGCGAATGCTGGCGCGGC----- 239
DB 135 CGAGCGGTGCGAGAGCTGCGCTCTGAGTACGTGACAGATGCTGGCGCGAGCGCC 194
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DB 195 CGGGGAGAGGCGGAGCCGGGAGCTGTCGCTCCGCGCTGCGCGAGCGCTGGCGCG 254
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QY 950 GCTGA 954
DB 905 GCTGA 909

RESULT 6
LOCUS MMU276871
DEFINITION Mus musculus mRNA for GDNF family receptor alpha 4, putative
ACCESSION AJ276871
VERSION AJ276871.1 GI:7688068
KEYWORDS alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Lindahl, M., Timmusk, T., Rossi, J., Saarna, M. and Airaksinen, M.S.
TITLE Expression and alternative splicing of mouse Gfra4 suggest roles in endocrine cell development
JOURNAL Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
MEDLINE 20319126
PUBMED 10860579

REFERENCE 2 (bases 1 to 882)
AUTHORS Airaksinen, M.S.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari 9), 00014 University of Helsinki, FINLAND

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ORIGIN

Query Match 62.6%; Score 630.6; DB 10; Length 882;
 Best Local Similarity 87.0%; Pref. No. 5, 1e-97;
 Matches 737; Conservative 0; Mismatches 84; Indels 26; Gaps 3;

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 Qy 948 CAGCTGA 954
 Db 876 CAGCTGA 882

RESULT 7

MMU276514 810 bp mRNA linear ROD 02-FEB-2001
 LOCUS Mus musculus mRNA for putative GDNF family receptor alpha 4,
 DEFINITION GPI-anchored isoform (Gfira4 gene).
 AJ276514

ACCESSION AJ276514.1 GI:7688056
 VERSION GDNF family receptor alpha 4; Gfira4 gene; GPI-anchored isoform.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 Lindahl, M., Timmusk, T., Rosei, J., Saarma, M. and Airaksinen, M.S.
 Expression and alternative splicing of mouse Gfira4 suggest roles in
 endocrine cell development
 Mol. Cell. Neurosci. 15 (6), 522-533 (2000)

JOURNAL MEDLINE 20319126
 PUBMED 10860579
 REFERENCE 2 (bases 1 to 810)
 AUTHORS Airaksinen, M.S.
 TITLE Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
 Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
 9), 00014 University of Helsinki, FINLAND

FEATURES

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Query Match 58.9%; Score 593.8; DB 10; Length 810;
 Best Local Similarity 90.2%; Pref. No. 8, 7e-91;
 Matches 650; Conservative 0; Mismatches 62; Indels 9; Gaps 1;

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DEFINITION	Sequence 2 from Patent WO0116169.			
ACCESSION	AX090389			
VERSION	AX090389.1 GI:13444248			
KEYWORDS				
SOURCE	Mus sp.			
ORGANISM	Mus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 Worley, D. Ret ligand 5 (rel15) from human and mouse Patent: WO 0116169-A 2 08-MAR-2001;			
AUTHORS	JOURNAL			
TITLE	BIOGEN, INC. (US)			
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Query Match 58.7%; Score 591.8; DB 6; Length 834;
Best Local Similarity 87.2%; Pred. No. 1.9e-90;
Matches 711; Conservative 0; Mismatches 62; Indels 42; Gaps 4;
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QY      888 TACTCAGTGGCTGGCTCTCCAGGCTGCTCTAA 922
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LOCUS      AX090395
DEFINITION      Sequence 8 from Patent WO0116169.
ACCESSION      AX090395
VERSION      AX090395.1 GI:13444253
KEYWORDS
SOURCE
ORGANISM
Mus sp.
Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Morley,D.
TITLE      Ret ligand 5 (retl5) from human and mouse
JOURNAL      Patent: WO 0116169-A 8 08-MAR-2001;
              BIOGEN, INC. (US)
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ORIGIN
Query Match      55.4%; Score 558.2; DB 6; Length 783;
Best Local Similarity 91.4%; Pred. No. 9,2e-85;
Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

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LOCUS      MMU276870
DEFINITION      Mus musculus mRNA for GDNF family receptor alpha 4, GPI-anchored
isoform (Gfra4 gene).
ACCESSION      AJ276870
VERSION      AJ276870.1 GI:7688066
KEYWORDS      alternative splicing; GDNF family receptor alpha 4; Gfra4 gene.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Lindahl,M., Timmusk,T., Rossi,J., Saarma,M. and Airaksinen,M.S.
TITLE      Expression and alternative splicing of mouse Gfra4 suggest roles in
JOURNAL      Mol. Cell. Neurosci. 15 (6), 522-533 (2000)
MEDLINE      20319126
PUBMED      10860579
REFERENCE      2 (bases 1 to 783)
AUTHORS      Airaksinen,M.S.
TITLE      Direct Submission
JOURNAL      Submitted (20-MAR-2000) Airaksinen M.S., Program in Molecular
Neurobiology, Institute of Biotechnology, P.O. Box 56 (Viikinkaari
9), 00014 University of Helsinki, FINLAND
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ORIGIN
Query Match      55.4%; Score 558.2; DB 10; Length 783;
Best Local Similarity 91.4%; Pred. No. 9,2e-85;
Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;

QY      124 GGGTCAGCAGCTCCACTGAGGGGAATCGCTGCTGAGACGCGAGCGTGCACAGCA 183
Db      46 GGGTCGCGAGCTTTACCGAGGGGAATCGCTGCTGAGACGCGAGCGTGCACAGCA 105

QY      184 GAGGACAGTGCAGCAGCTGCTCCGATGATGCTGCGCAATGCTTGGGCGGCGC---- 229
Db      106 GACGAGGAGTGCAGCAGCTGCTGAGATGCTGCAAGATGCTGCGGCGGCGAGCG 165

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misc_feature	1..46	/note="Corresponds to exon 1 (11113 to 11158) of Seq ID 1"
misc_feature	47..414	/note="Corresponds to exon 2 (12443 to 12810)"
misc_feature	415..502	/note="Corresponds to exon 3 (12882 to 12969)"
misc_feature	503..637	/note="Corresponds to exon 4 (13051 to 13185)"
misc_feature	638..718	/note="Corresponds to exon 5 (13726 to 13806)"
misc_feature	719..795	/note="Corresponds to exon 6 (13876 to 13993)"
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Best Local Similarity	88.5%; Pred. No. 1e-76;	
Matches	587; Conservative 0; Mismatches 49; Indels 27; Gaps 2;	
QY	124 GGGTCAGCGAGCTCCACTGAGGAGAAATTCGCTGCTGGAAAGCAGCGGCTGTGACACGA	183
DB		
QY	46 GGGTCGTGGACCTTACCGACGGGAAATCGCTGCTGGACGGGGCCGAGGCTGTGACACGA	105
DB		
QY	184 GACGAGCAGTGCACGACAGCTCGGCTCGAGTACGTGGGCGCAATGCTGTGGGCGGGG----	239
DB	106 GACGAGCGGTGTCGACGACAGTGCCTCTGAGTACGTGGACCAATGCTGTGGGCGGGGACG	165
QY	240 -----GGGCTTGGCGGGGACCCGGGAGCTGCCTGCTCCGCTCGCGCGCTGCTCGG	294
DB	166 CCGGGGGGACAGCGCGGAGCCCGGGGGGTGGGTGGCTCCGCTCGCGCGAGCCCTTGGC	225
QY	295 CGCTTCTTTCGCGCGGGGCTTCGGGCGCTCACGCACGGCGTCTTCTTCTGCGATGCGAA	354
DB	226 CGCTTCTTTCGCGCGTGGGGCTTCGGGCGCTCACGATGCGTCTTCTTCTGCGGCTGCGAA	285
QY	355 GCGCCCGCGTGGCGCGGAGCGCGGCGCGCAGACATTCGCGCCCGCTGGCGGCTTTCGCGC	414
DB	286 GGGTCGCGGTGCGCGGAGCGCGCGCGCAGACCTTTCGCGCCCGCTGGCGGCTTTCGCGC	345
QY	415 CCCGAGCTGGCGGCACCTTCTGTGCTGAAGCCTTGGACGCTGCGAGCGAAGCGCGCG	474
DB	346 CCGGGGTTTGTGTGCGCCCTCTTGTGCTGAAGCCCTTGAAGCGCTCGAGCGGACGCGCTG	405
QY	475 TGGCGGCGCCGCTCTTGTTCCTTCCAGGCTCATGCGCTCCGCGCGCCCGGCTCCCGGAC	534
DB	406 TGGCGGTGC-----GCTCATGCGCTCCGCGCGCGGCTCCCGGAC	447
QY	535 GCGTGTCCGAGAGAGGGGGGCGCGCGGTGTGTGGCGCCTTACGAGGCTTGTATGCAAC	594
DB	448 CGCTGCCCGAGAGGGGGGCGCGCGGTGTGTGGCGCTTACGAGGCTTATATGGCAAC	507
QY	595 GTGGTCAACCCCACTACTGGAACAAGTGAGCGCGCGCTTGGGACCTGTGTGGCGGTGT	654
DB	508 GTGGTCAACCCCACTACTGGAACAAGTGAGCGCGCGCTTGGGACCTGTGTGGCGGTGT	567
QY	655 GAGGCCAGCGGAAACCGGCGGGAAGTGCAGACCTTCCGCAAGCTTTTACAAAGAAAC	714
DB	568 GCGGCGAGTGGAACCGGCGGGAAGTGCAGACCTTCCGCAAGCTTTTACAAAGAAAC	627
QY	715 CCGTGTGTGATGTGTGATCAACAAGCCTTTTGAACGCTTGCAACAATCAAGTTCTGAGAAC	774
DB	628 CCGTGTGTGATGTGTGATCAACAAGCCTTTTGAACGCTTGAGCATAGTTCTTGCAGAAC	687
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RESULT 12		
AX068323	2522 bp	DNA linear PAT 25-JAN-2001
LOCUS	AX068323	
DEFINITION	Sequence 5 from Patent WO0102557.	
ACCESSION	AX068323	
VERSION	AX068323.1	GI:12578506

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Rattus rattus (black rat)
Rattus rattus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1
Masure, S.L., Cik, M. and Hofnagel, E.W.
Neurotrophic factor receptor gfr-alpha-4
Patent: WO 0102557-A 5 11-JAN-2001,
JANSSEN PHARMACEUTICA N.V. (BE)

location/Qualifiers
1. 2522
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ORIGIN

Query Match 45.1%; Score 454.4; DB 6; Length 2522;
Best Local Similarity 82.3%; Pred. No. 2,7e-67;
Matches 604; Conservative 0; Mismatches 1; Indels 129; Gaps 2;

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743 AGACGACAGCTGCGACGAGCTGCGCTCCAGTACGTGCGCAATGCTTGGCGCGGCGG 802
243 CTGGCGGGGACCGCGGAGCTGCTGCGCTCCCGTGGCGCGCTGCGCGCTTCTT 302
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303 CGCGCGGGGCTCCCGGCGCTGCGACGAGCGCTCTTCTGGGGAATGGAAGGCGCGC 362
863 CGCGCGGGGCTCCCGGCGCTGCGACGAGCGCTCTTCTGGGGAATGGAAGGCGCGC 922
363 GTGCGCGGAGCGCGGCGCGACGATTCGCGCGCGCTTCTCCGCGCGCGACGCT 422
923 GTGCGCGGAGCGCGGCGCGACGATTCGCGCGCGCTTCTCCGCGCGCGACGCT 982
423 GGGCGCACCTTCTGCTGAGCGCTTGAAGCGCTTGAAGCGCGCGCGGCGGCGGCGG 478
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1103 CTTTCCAGGCTCATGCGCTCCGCGCGCGCTCCGCGAGCGCTTCCGAGAGAGGCGG 1162
554 GCGCGGCTGCTGCGCGCTTGAAGCGCTTGT----- 587
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714 CCGCTGCTTGGATG 727
1403 CCGCTGCTTGGATG 1416

RESULT 13
AC094932
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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Rattus norvegicus clone CH230-6D19, *** SEQUENCING IN PROGRESS ***.
AC094932
AC094932.5 GI:30466943
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 245589)
Muzny, D., Marie, J., Metzker, M., Lee, J., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D., Anyalebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benham, F., Bissell, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Huylk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpethy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheue, L., Louleget, H., Lozada, R.J., Lu, X., Ma, D., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundae, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackeleme, O., Okunolu, G., Olamunagbon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, A., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinsley, A., Trejos, Z., Uman, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, Y., Zhou, J., Zhou, S., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 245589)
Worley, K.C.
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245589)

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Qy	714	CCCTGCTTGGAGT 727	
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LOCUS			linear
DEFINITION	Homo sapiens GFR receptor alpha 4 protein (GFRAL4)	mRNA, complete	
ACCESSION	AF253318		
VERSION	AF253318.1	GI:10998399	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1427)		
AUTHORS	Zhou, B., Levinson, B. and Gitschier, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-APR-2000) Department of Medicine, University of California, 533 Parnassus Ave, San Francisco, CA 94143, USA		
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CDS

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ORIGIN

Query Match 42.7%; Score 430.6; DB 9; Length 1427;
 Best Local Similarity 73.2%; Pred. No. 3.2e-63;
 Matches 595; Conservative 0; Mismatches 184; Indels 34; Gaps 2;

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184 GAGGAGCAGTCCAGCAGCTGCGCTCCGAGTACGTGGCGCAATGCTGGGCGGAGCG 243
106 GAGCGCGGAGTCCAGCAGCTTGGCTCGAGTATGTGCGAGTCCGCGGCGCGGCG 161
244 TGCGGGGAGCCGCGAGCTGCTGCGCTCCGCGTCCGCGCGCGCTGCGCGCTTTC 303
162 -----TGCAGAGGGGGGCTGTCCCGCGCGCGCGCGCGCGCGCTTTC 216
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424 GCGCGAGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 483
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Db 792 TCTCCGCGCGCTGCTGATTAAGACAGCGAC 824

RESULT 15
 HSA291673
 LOCUS
 DEFINITION
 Homo sapiens mRNA for GDNF family receptor alpha 4, GPI anchored isoform (GFR4 gene).

ACCESSION
 AJ291673
 VERSION
 AJ291673.1 GI:12038956
 KEYWORDS
 GDNF family receptor alpha 4, GPI anchored isoform; Gfr4 gene.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE

AUTHORS

TITLE

Human glial cell line-derived neurotrophic factor receptor alpha 4 is the receptor for persephin and is predominantly expressed in normal and malignant thyroid medullary cells

JOURNAL

MEDLINE

PUBMED

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REMARK

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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REMARK

REFERENCE

AUTHORS

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JOURNAL

MEDLINE

PUBMED

REMARK

REFERENCE

AUTHORS

TITLE

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Db 517 CTTAACTAGTGAACAAGTCGAGCGCGGCTTGGGCGCTTGTGCGGCTGTGAGGCGAC 576
OY 664 GGAACCGGCGGAGAGTCGGAAGCTTCCGCAAGCTTTTACAAGAACCCCTGCTTG 723
Db 577 GGGAACTGGGCTGAGGACTGCGAAGCTTCCGGGGCTCTTTACAGGAACCGTGTG 636
OY 724 GATGTCATACAGCTTTGACAGCTGCAACCATCAGTCTTGCAGGACCAAGTGAAC 783
Db 637 GATGTCATACAGCTTTGACAGCTTGCAGGCGGGTGGCCCCCAAGTCTGTGACCAAGTGAAC 696
OY 784 CCTTACAGAAATGCTGGGCAAGGCCAAGGTGAAG 817
Db 697 CCGCAGGAGAACCGGAGCACAGCTCTGCGAGG 730

Search completed: February 18, 2005, 02:49:21
Job time : 4695 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 00:54:05 ; Search time 698 Seconds
(without alignments)
8548.853 Million cell updates/sec

Title: US-10-019-337e-7
Perfect score: 1008
Sequence: 1 ctggttaagcttaagcaga.....aactccttgccctcagtc 1008

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2359870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1008	100.0	1008	4	AAf31063 Rat GFRal
2	872	86.5	953	4	AAf31062 Rat GFRal
3	630.6	62.6	882	4	ABLS1670 Mouse put
4	591.8	58.7	834	4	AAf57270 Mouse Ret
5	558.2	55.4	783	4	AAf57273 Mouse Ret
6	558.2	55.4	783	4	ABLS1669 Mouse GPI
7	510.6	50.7	795	4	AAf57271 Mouse Ret
8	487.2	48.3	1019	2	AAf28259 Murine gl
9	454.4	45.1	2522	4	AAf31061 Rat GFRal
10	427.6	42.4	810	4	ABLS1672 Human GPI
11	427.4	42.4	849	4	AAf57272 Human Ret
12	356.8	35.4	15914	4	AAf57269 Mouse Ret
13	320.8	31.8	900	4	ABLS1673 Human put
14	313.6	31.1	573	4	ABLS1671 Mouse sec
15	299.6	29.7	995	4	AAf31039 Mouse cdu
16	299.6	29.7	995	6	ABLS1675 Murine CD
17	291.4	28.9	549	4	ABLS1674 Human put
18	284	28.2	901	4	AAf31059 Rat clone
19	258.8	25.7	792	4	AAf31057 Murine ES
20	216.8	21.5	2047	4	ABLS1675 Human GFR

c	21	216.4	21.5	207433	5	ABZ72040	ABZ72040 Gene 216
c	22	216.4	21.5	207433	8	ABX74891	ABX74891 BAC1098L2
c	23	216.4	21.5	207433	12	ADJ36614	Adj36614 Bacterial
c	24	216.4	21.5	207433	12	ADL81193	Adl81193 BAC1098L2
	25	213.4	21.2	346	4	ABLS1689	ABLS1689 Human GFR
	26	209	20.7	872	4	AAf31060	AAf31060 Rat clone
	27	202	20.0	497	4	AAf31058	AAf31058 Murine ES
	28	150.4	14.9	1392	3	AAZ91456	AAZ91456 Human neu
	29	150.4	14.9	1392	6	ABN87349	ABN87349 Human neu
	30	150.4	14.9	1392	6	ABK50453	ABK50453 Human neu
	31	150.4	14.9	1392	10	ADD11683	Add11683 Human neu
	32	150.4	14.9	1490	2	AAx01741	Aax01741 Human GDN
	33	150.4	14.9	1543	2	AAV64342	AAV64342 Human TGF
	34	150.4	14.9	1543	2	AAV99332	AAV99332 Glial cel
	35	150.4	14.9	1646	5	AAf64145	AAf64145 Nucleotid
	36	150.4	14.9	1646	5	AAf98442	AAf98442 Human CDN
	37	150.4	14.9	1888	2	AAV00248	AAV00248 Human Ret
	38	150.4	14.9	1888	12	ADJ58704	Adj58704 Human Ret
	39	150.4	14.9	1995	2	AAV58006	AAV58006 Human neu
	40	150.4	14.9	1995	3	AAZ91459	AAZ91459 Human NTN
	41	150.4	14.9	1995	6	ABN87360	ABN87360 Human NTN
	42	150.4	14.9	1995	6	ABL41778	ABL41778 DNA seque
	43	150.4	14.9	1995	6	ABK50456	ABK50456 Human NTN
	44	150.4	14.9	1995	10	ADD11666	Add11666 Human NTN
	45	150.4	14.9	2600	2	AAV58004	AAV58004 Human neu

ALIGNMENTS

RESULT 1
ID AAF31063 standard; CDNA; 1008 BP.
XX
AC AAF31063;
XX
DT 06-APR-2001 (first entry).
XX
PR Rat GFRalpha-4 splice variant B coding sequence.
XX
DE Rat GFRalpha-4; carcinoma; familial hirschsprung disease; pain;
XX
KW glial cell-line derived neurotrophic factor; neurodegenerative disease;
KW GDNF family receptor alpha-4; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; peripheral neuropathy; spinal cord injury;
KM chromosome 3q36; ss.
XX
OS Rattus rattus.
XX
PN W0200102557-A1.
XX
PD 11-JAN-2001.
XX
PF 26-MAY-2000; 2000WO-EP004918.
XX
PR 29-JUN-1999; 99GB-00015200.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Measure SLT, Ctk M, Hoefnagel EW;
XX
WP: 2001-138137/14.
DR P-PSDB; AAB61637.
XX
PT Glial cell-line derived neurotrophic factor family receptor alpha-4,
PT useful for preparing medicaments for treating neurodegenerative diseases
PT (e.g. Alzheimer's disease, Parkinson's disease) and carcinomas.
XX
BS Claim 6; Page 72-73; 82pp; English.
XX
CC The present invention relates to rat Glial cell-line Derived Neurotrophic
CC Factor (GDNF) family receptor alpha-4 (GFRalpha-4; see AAB61636 and
CC AAB61637). The present sequence is the coding sequence for rat GFRalpha-4
CC splice variant B. GFRalpha-4 is useful in the preparation of a medicament


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Db 121 AGAGGCTCAGGAGCTCCACTGAGAGGGAGATCGCTGCTGAGAGCAGCCGAGCGTGACA 180
Qy 181 GCGAGAGAGAGTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 240
Db 181 GCGAGAGAGAGTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 240
Qy 241 GCGTGGGGGAGACCGGGAGAGCTGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 300
Db 241 GCGTGGGGGAGACCGGGAGAGCTGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 300
Qy 301 TTGCGCGCGGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 360
Db 301 TTGCGCGCGGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 360
Qy 361 GCGTGGCGGAGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 420
Db 361 GCGTGGCGGAGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 420
Qy 421 CTGGCGCGGAGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 480
Db 421 CTGGCGCGGAGAGCTCCGAGAGCTGCGCTCCGAGAGTGGGAGCAATGCTGGGCGGGGCG 480
Qy 481 CCGCGTCTTTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 540
Db 481 CCGCGTCTTTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 540
Qy 541 CCGGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 600
Db 541 CCGGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 600
Qy 601 ACCCGCAACTACCTGAGCAAGAGTGGGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTT 660
Db 601 ACCCGCAACTACCTGAGCAAGAGTGGGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTT 660
Qy 661 AGCGGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 720
Db 661 AGCGGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 720
Qy 721 TTGATGCTGCTATCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 780
Db 721 TTGATGCTGCTATCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 780
Qy 781 AACCCCACTACCTGAGCAAGAGTGGGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTT 840
Db 781 AACCCCACTACCTGAGCAAGAGTGGGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTT 840
Qy 841 GAGGAGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 900
Db 841 GAGGAGAGAGAGGGGGCGCGCGGCTGCTGCGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 900
Qy 901 GCGTCTCAGAGCGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 960
Db 846 GCGTCTCAGAGCGCTGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 905
Qy 961 TGTCTCTGAGTATGCTCACTGAACTGAAACTCCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 1008
Db 906 TGTCTCTGAGTATGCTCACTGAACTGAACTCCCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 953

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KW medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia;
KM neuronal disorder; aberrant axonal sprouting; gene; ss.
XX Mus musculus.
OS
FH Key Location/Qualifiers
FT CDS 1..882
FT /tag= a
FT /product= "transmembrane isoform a2"
XX
XX WO200162795-A1.
XX
XX 30-AUG-2001.
XX
XX 14-NOV-2000; 2000MO-F1000994.
XX
XX 21-FEB-2000; 2000FI-00000394.
XX
XX (LICE-) LICENTIA LTD.
XX
XX Alrakainen M, Saarna M, Poterjiaev D, Lindahl M, Timmusk T,
XX Rossi J;
XX
XX WPI; 2001-596722/67.
XX
XX P-PsDB; ABB09215.
XX
XX
XX New nucleic acid sequence for manufacturing polypeptides for treating
XX PT endocrine cancers comprises a cDNA encoding a splicing isoform of
XX PT mammalian growth factor receptor (GFR) alpha4.
XX
XX
XX Claim 4; Fig 19A; 143pp; English.
XX
XX
XX The present invention describes an isolated and purified cDNA sequence
XX CC encoding a splicing isoform of a mammalian growth factor receptor
XX CC (GFR) alpha4, or its fragments. GFRalpha4 sequences have cytosolic,
XX CC osteopathic, neuroprotective and anticonvulsant activities. GFRalpha4 is
XX CC a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived
XX CC neurotrophic factor (GDNF) family alpha-receptor. A GFRalpha4
XX CC polynucleotide sequence can be used for recording GFRalpha4 mediated
XX CC signalling in neurons or endocrine cells such as thyroid calcitonin-
XX CC producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or
XX CC cells from the pituitary intermediate lobe. GFRalpha4 protein and
XX CC polynucleotide sequences can be are used for manufacturing polypeptides
XX CC useful for diagnosing and/or treating tumours in parathyroid gland cells,
XX CC adrenal chromaffin cells, cells of pituitary intermediate lobe,
XX CC neoplasia, endocrine tumours, medullary thyroid carcinoma and
XX CC pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for
XX CC preventing neuronal death or aberrant axonal sprouting. The present
XX CC sequence encodes the mouse GFRalpha 4 protein, designated transmembrane
XX CC isoform a2, from the present invention.
XX
XX
XX Sequence 882 BP; 121 A; 303 C; 296 G; 162 T; 0 U; 0 Other;
XX
XX
XX Query Match 62.6%; Score 630.6; DB 4; Length 882;
XX Best Local Similarity 87.0%; Pred. No. 7.9e-125;
XX Matches 737; Conservative 0; Mismatches 84; Indels 26; Gaps 3;
Qy 124 GGGTCAAGCAGCTCACTGAGAGGGGAATCGCTGCTGAGAGCAGCCGAGCGTGCACAGCA 183
Db 46 GGGTCTGCGAGCTTTTACGAGCGGGAATCGTGGGTGAGACCGCGGCGAGGCTGACAGCA 105
Qy 184 GACGAGCAGTGCAGCAGCTGCGCTCCGAGTACGTGGCGGAATGCTTGGGCGGGC----- 239
Db 106 GACGAGCGTGCAGCAGCTGCGCTCCGAGTACGTGGCGGAATGCTTGGGCGGGCAGCG 165
Qy 240 -----GGGCTGGCGGGGACCGGGAGCTGCTGCGCTCCGCTGCGCGCGCTGCGCGCG 294
Db 166 CCGCGGGGCGAGCGCGGAGACCGGGAGCTGCTGCGCTCCGCTGCGCGCGCGCGCGCG 225
Qy 295 CGCTTCTTCCGCGCGCGGCTTCCGCGCTCAGCAGCAGCGGCTCTTCTGCGGATGCGAA 354
Db 226 CGCTTCTTCCGCGCGCGGCTTCCGCGCTCAGCAGCAGCGGCTCTTCTGCGGATGCGAA 285

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QY 355 GGGCCCGCGTGCAGCGCCGCGCCAGACATTCGCGCCGCTTCGCGCTTCGCGC 414
DB 286 GGGTCGCGCGTGCAGCGCCGCGCCAGACATTCGCGCCGCTTCGCGCTTCGCGC 345
QY 415 CCCCACTGGCGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 474
DB 346 CCGGGGTGGTGGCGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 405
QY 475 TGGCGGCGCGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 534
DB 406 TGGCGGCGCGGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 465
QY 535 GGGTGTCCGAGAGAGGGGGGCGCGGTGTCTGCGCGCTTCGAGCGCTTCGAGCGCC 594
DB 466 CGCTGCGCGAGAGAGGGGGGCGCGGTGTCTGCGCGCTTCGAGCGCTTCGAGCGCC 525
QY 595 GTGGTACCCCGCACTACCTGAGACACGTAGAGCGCGCGCTTCGCGCTTCGAGCG 654
DB 526 GTGGTACCCCGCACTACCTGAGACACGTAGAGCGCGCGCTTCGCGCTTCGAGCG 585
QY 655 GAGCGCCAGCGAAGCGGCGCGAAGAGTGCAGAGCTTCGCAAGCTTTTACAGAGAC 714
DB 586 GCGGCGAGTGCAGAACCGGCGCGAAGATGCAAGCTTCGCAAGCTTTTACAGAGAC 645
QY 715 CCCTGTGGATGTGTCATACAGAGCTTCGAGCGCTTCGCAAGCTTCGAGAGAC 774
DB 646 CCCTGTGGATGTGTCATACAGAGCTTCGAGCGCTTCGAGCGCTTCGAGAGAC 705
QY 775 CAGTGAACCCCTACCAAGATGCTGGGCGAGCCCAAGGTGAGAGCTTCGAGCGCT 834
DB 706 CAG-----ACTGCTGGGTGCTGTTCCTCCGCGGCAAGGACAGAGGCTTAGAA 755
QY 835 GAGATGAGAGCAGAAACGTCCTCCGTTTGT-----CCCAAGTGTCTCGATGCCA 887
DB 756 GAGCTGAGAGCAAAACAGTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 815
QY 888 TACTCACTGCGCTGCTTCAGGCGCTGCTTAATTGAGAGGTGAACCATGAGACAA 947
DB 816 CACTCACTGCGCTGCTTCAGGCGCTGCTTGAATTGAGAGCATGAACGTGAGACAA 875
QY 948 CAGCTGA 954
DB 876 CAGCTGA 882

```

RESULT 4

AAFS7270
ID AAF57270 standard, cDNA, 834 BP.

AC AAF57270;

DT 29-MAY-2001 (first entry)

XX Mouse RetL5 polypeptide encoding cDNA.

XX Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephropathic;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
KM vulnerable; neurotrophic; anti-HIV; neuroprotective; antibacterial; ss;
KM cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 1..834

FT /*tag= a

FT /*product= "RetL5"

FT sig_peptide 1..63

FT /*tag= b

FT mat_peptide 64..831

FT /*tag= c

XX MO200116169-A2.

```

PD 08-MAR-2001.
XX
XX 01-SEP-2000; 2000WO-US024111.
PF
XX 01-SEP-1999; 99US-0152024P.
PR
XX (BIOI) BIOGEN INC.
PA
XX
XX Worley D;
PI
XX WPI: 2001-235091/24.
DR
XX P-PSDB; AAB62103.
DR
XX
XX Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT cell that expresses Ret and for modulating Ret signal transduction
PT involving a cell expressing Ret polypeptide or Ret ligand polypeptide.
XX
XX Claim 1, Fig 1; 76pp; English.
XX

```

The invention relates to mouse and human Ret ligand 5 (RetL5) polypeptides. The RetL5 polypeptides can be expressed by standard recombinant methodology. The RetL5 when bound to Ret, acts as a dimerization or autophosphorylation activator. The polypeptides and their antibodies are useful for stimulating growth of or limiting damage to, Ret expressing tissue in a subject, for suppressing growth of a tumour cell that expresses Ret, for modulating Ret signal transduction involving a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion proteins containing RetL5 and antibodies are useful for stimulating renal tissue growth and/or survival, supporting renal function and minimizing damage to renal tissue after various insults, particularly for treating acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic injury and trauma. The compounds are also useful for treating conditions such as neural degeneration where neural growth and regeneration are desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as motor neuron disease, demyelinating disease, bacterial diseases, viral diseases, and prion diseases including Creutzfeldt-Jakob disease. The compounds are also useful for treating disorders due to damage to neural tissue caused by neoplastic implantment, trauma or cerebrovascular events such as hemorrhage or emboli, and neural disorders such as mental retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral palsy. The present sequence represents the mouse RetL5 cDNA sequence predicted by visual inspection method

SO Sequence 834 BP; 110 A; 291 C; 281 G; 152 T; 0 U; 0 Other;

Query Match 58.7%; Score 591.8; DB 4; Length 834;

Best Local Similarity 87.2%; Pred. No. 1.4e-116;

Matches 711; Conservative 0; Mismatches 62; Indels 42; Gaps 4;

```

QY 124 GGGTCAGCAGCTCCACTGAGGGGAATGCTGCTGAGGAAGACGAGCGGTGCACAGCA 183
DB 46 GGGTCGCAAGCTTTTCCAGCGGAATCGCTCGTGAAGCGAGCGAGCGGTGACGA 105
QY 184 GACGACAGTGCAGAGAGTGCCTCGAGTACGTGCGCAATGCTTCGCGCGAGC---- 239
DB 106 GACGACAGTGCAGAGAGTGCCTCGAGTACGTGCGCAATGCTTCGCGCGAGAGG 165
QY 240 -----GGGCTGCGGAGACCGGAGCTGCTGCGCTCCGCTGCGCGCTGCGCGC 294
DB 166 CCGGAGGAGCAGGCGCGGACCCGAGGCTGCTGCTGCGCTGCGCGCGAGACCGCTGCGC 225
QY 295 CGCTTTTTCGCGCGGAGCTTCGCGCTGCAAGACGCGCTCTTCGCGAGTGCAG 354
DB 226 CGCTTTTTCGCGCGGAGCTTCGCGCTGCAAGACGCGCTCTTCGCGAGTGCAG 285
QY 355 GGGCCGCGTGCAGAGCGCGAGCGCGAGCATTTGCGCGCGCTGCGCGCTTCGCGC 414
DB 286 GGGTCGCGTGCAGAGCGCGAGCGCGAGCATTTGCGCGCGCTGCGCGCTTCGCGC 345
QY 415 CCCAGCTGCGCGCACTTCCTGAGAGCCCTTGAGACCGCTGCGAGGAAACCGCGCG 474

```

cell, that expresses Ret and for modulating Ret signal transduction
 involving a cell expressing Ret polypeptide or Ret ligand polypeptide.
 Disclosure, Fig 7, 76pp, English.

The invention relates to mouse and human Ret ligand 5 (RetL5)
 polypeptides. The RetL5 polypeptides can be expressed by standard
 recombinant methodology. The RetL5 when bound to Ret, acts as a
 dimerization or autophosphorylation activator. The polypeptides and their
 antibodies are useful for stimulating growth of or limiting damage to,
 Ret expressing tissue in a subject, for suppressing growth of a tumour
 cell that expresses Ret, for modulating Ret signal transduction involving
 a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion
 proteins containing RetL5 and antibodies are useful for stimulating renal
 tissue growth and/or survival, supporting renal function and minimizing
 damage to renal tissue after various insults, particularly for treating
 acute renal failure, acute nephritis, chronic renal failure, nephrotic
 syndrome, renal tubule defects, kidney, transplants, toxic injury, hypoxic
 injury and trauma. The compounds are also useful for treating conditions
 such as neural degeneration where neural growth and regeneration are
 desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
 disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
 motor neuron disease, demyelinating disease, bacterial diseases, viral
 diseases, and prion diseases including Creutzfeldt-Jakob disease. The
 compounds are also useful for treating disorders due to damage to neural
 tissue caused by neoplastic impingement, trauma or cerebrovascular events
 such as hemorrhage or emboli, and neural disorders such as mental
 retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
 palsy. The present sequence represents an alternatively spliced mouse
 RetL5 encoding cDNA

Sequence 783 BP, 92 A, 280 C, 266 G, 145 T, 0 U, 0 Other:

	Matches	606:	Conservative	0:	Mismatches	48:	Indels	9:	Gaps	1:
QY	124	GGGTACAGGAGCTCACTGAGGGGAATCGCTGCTGGAGACGCGGAGCGTGCACAGCA	183							
Db	46	GGGTCTGTGGAGCTTAACTCCGACGGGAATCGCTGCTCGTAGACGGCGCCGAGGCTCTTGACAGCA	105							
QY	184	GACGAGCAGTGCAGACAGCTGCCTCCGAGTACGTGGGCGCAATGCTCTGGGCGGGAGC----	239							
Db	106	GACGAGCGGTATCCAGCAGACTGCCTCTGAGTACGTGGCACGATGCTTGAGGCGGGAGCAGCG	165							
QY	240	-----GGGCTTGGCGGGGAACCCGGAGCTGCGTGGCTCCCGCTGCGCGCTGGCTTGGC	294							
Db	166	CCGGGGGACAGGCGCGGAGCCGGGGGGCTGCGTGGCTCCGCTCCGCGCTCGCGCGAGCCCTGGCG	225							
QY	295	CGCTTTCTTGGCGCGCGGGGCTTCGCGCGCTACAGACCGCTGCTCTTGTGGATGAGAA	354							
Db	226	CGCTTCTTGGCGCGCTGGGCTCTCGGCGCTACGATGCGCTCTTCTTGTGGGCTGGCAAA	285							
QY	355	GGCCCGCGGTGCGCGAGCGCGCGCGCAGACATTCCGCGCCGCGCTGCGCTTCTCCGGC	414							
Db	286	GGCTTCGCGTGGCGCGAGCGCGCGCGCCAGACTTTCGCGCCCGCTGCGCTTCTCCGGC	345							
QY	415	CCCAAGCTGCGCCACTTCTCTGCTTGAAGCCTTGGACCGCTGCGAGACGACCGCGCG	474							
Db	346	CCGGGGTGTGGCGCGCGCTCTTGTGCTGAGAGCCCTGGAGCGCTGCGAGCGGACGCGCTG	405							
QY	475	TGCGGGCGCGCGTCTCTTGGCTTCCAGGCGCTCATGCGCTCCCGAGCGCGGCTCCCGGAC	534							
Db	406	TGCGGCGCGCGCTCTCTTGAAGCGCTCATAGCGCTCCCGGCGCGCGCTTCCCGGAC	465							
QY	535	GGCTGTCCGAGAGAGGGGGGCGCGCGGTGTCTGCGCGCTTACGAGGCGCTTGTAGCAAC	594							
Db	466	CGTGGCGCGAGAGGGGGGCGCCCGCTGTGTCTTGCGCGCTTACGAGGCGCTCATAGGACAC	525							
QY	595	GTGATCACCCCAACTACTGTGACAAAGTGAAGCGCGCGGTGGCGCGCTGGTGGGCGCTGT	654							
Db	526	GTGATCACCCCAACTACTGTGACAAAGTGAAGCGCGCGCGCTGGTGGGCGCGCTGT	585							

QY 655 GAGGCCAGCGAAACCGGCGCGGAAGTGGGAAGCTTCCGCAAGCTTTTACAGAGAC 714
 Db 586 GCGCCAGTGTGAACCGGCGCGGAAGTGGGAAGCTTCCGCAAGCTTTTACAGAGAC 645
 QY 715 CCCTGCTGGATGTGCATACAGCCTTTCAGACGTCGCAACCATCAGTTCTGCAGGAC 774
 Db 646 CCCTGCTGGATGTGCATACAGCCTTTCAGACGTCGCAACCATCAGTTCTGCAGGAC 705
 QY 775 CAG 777
 Db 706 CAG 708
 RESULT 6
 ABL51669
 ID ABL51669 standard; cDNA; 783 BP.
 XX ABL51669;
 AC 08-JUL-2002 (first entry)
 XX Mouse GPI-anchored isoform a1 encoding cDNA SEQ ID NO:7.
 DE
 XX
 XX GFRalpha4; glycosyl-phosphatidylinositol; GPI; GDNF; cytosolic;
 KM glycosyl-phosphatidylinositol-linked GDNF family alpha-receptor;
 KM glial cell line derived neurotrophic factor; osteopetrotic; tumour;
 KM neuroprotective; anticonvulsant; neoplasia; endocrine tumour;
 KM medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia;
 KM neuronal disorder; aberrant axonal sprouting; gene; ss.
 XX
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 1..783
 FT /tag= a
 FT /product= "GPI-anchored isoform a1"
 FT
 FT WO200162795-A1.
 XX
 XX 30-AUG-2001.
 PD 14-NOV-2000; 2000MO-FI000994.
 XX
 XX 21-FEB-2000; 2000FI-00000394.
 PR
 PA (LICE-) LICENTIA LTD.
 XX
 PI Alraksinen M, Saarna M, Poterjasev D, Lindahl M, Timmusk T;
 PI Rossi J;
 DR WPI; 2001-596722/67.
 DR P-SDB; ABB09214.
 XX
 PT New nucleic acid sequence for manufacturing polypeptides for treating
 PT endocrine cancers comprises a cDNA encoding a splicing isoform of
 PT mammalian growth factor receptor (GFR)alpha4.
 PT
 PS Claim 4; Fig 18A; 143pp; English.
 XX
 XX The present invention describes an isolated and purified cDNA sequence
 CC encoding a splicing isoform of a mammalian growth factor receptor
 CC (GFR)alpha4, or its fragments. GFRalpha4 sequences have cytosolic,
 CC osteopetrotic, neuroprotective and anticonvulsant activities. GFRalpha4 is
 CC a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived
 CC neurotrophic factor (GDNF) family alpha-receptor. A GFRalpha4
 CC polynucleotide sequence can be used for recording GFRalpha4 mediated
 CC signaling in neurons or endocrine cells such as thyroid calcitonin-
 CC producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or
 CC cells from the pituitary intermediate lobe. GFRalpha4 protein and
 CC polynucleotide sequences can be used for manufacturing polypeptides
 CC useful for diagnosing and/or treating tumours in parathyroid gland cells,
 CC adrenal chromaffin cells, cells of pituitary intermediate lobe,
 CC neoplasia, endocrine tumours, medullary thyroid carcinoma and

CC pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for
 CC preventing neuronal death or aberrant axonal sprouting. The present
 CC sequence encodes the mouse GFRalpha 4 protein, designated GPI-anchored
 CC isoform a1, from the present invention
 CC
 XX
 SQ Sequence 783 BP; 92 A; 280 C; 266 G; 145 T; 0 U; 0 Other;
 Query Match 55.4%; Score 558.2; DB 4; Length 783;
 Best Local Similarity 91.4%; Pred. No. 2,1e-109;
 Matches 606; Conservative 0; Mismatches 48; Indels 9; Gaps 1;
 QY 124 GGGTCAGCGAGCTCCACTAGAGGGAATCGCTCGTGTGGAAGCGGAGCGGTGACAGCA 183
 Db 46 GGGTCAGCGAGCTCCACTAGAGGGAATCGCTCGTGTGGAAGCGGAGCGGTGACAGCA 105
 QY 184 GACGAGCAGTGCAGAGCTGCGCTCCGAGTACGTGAGCAATGCTGTGGGCGGAGC---- 239
 Db 106 GACGAGCAGTGCAGAGCTGCGCTCCGAGTACGTGAGCAATGCTGTGGGCGGAGC 165
 QY 240 -----GGGCTGAGCGAGGAGCCGAGAGCTGCGCTCCGCTGCGCGCGCTGCGC 294
 Db 166 CCGGAGGAGGAGCGGAGCCGAGAGCTGCGCTCCGCTGCGCGCGCTGCGC 225
 QY 295 CGCTTCTTGCCCGCGGAGCTCCGAGTACGAGCAAGCGCTGCTTCTGCGAGTGCAG 354
 Db 226 CGCTTCTTGCCCGCGGAGCTCCGAGTACGAGCAAGCGCTGCTTCTGCGAGTGCAG 285
 QY 355 GGGCGGCGCTGCGCGAGGCGCGGCGCGAGCATTCGCGCGCGCTGCGCTGCGC 414
 Db 286 GGGCGGCGCTGCGCGAGGCGCGGCGCGAGCATTCGCGCGCGCTGCGCTGCGC 345
 QY 415 CCGCAGCTGAGCGCGACCTTCTGCTGAGAGCCCTTGAACCGCTGCGAGGAGCGCGC 474
 Db 346 CCGGAGGAGTGTGCGCGCTTGTGCTGAGAGCCCTTGAACCGCTGCGAGGAGCGCGC 405
 QY 475 TGGCGGCGCGCTGCTTCTTTCCTTCAGAGGCTATAGGCTCCGCGCGCGCTCCGCGAG 534
 Db 406 TGGCGGCGCGCTGCTTCTTTCCTTCAGAGGCTATAGGCTCCGCGCGCGCTCCGCGAG 465
 QY 535 GGGCTGCGAGGAGGAGGAGGCGCGGCTGCTGCGCGCTTACGAGAGCTTGTAGGAGC 594
 Db 466 CGCTGCGCGAGGAGGAGGAGGCGCGGCTTGTGCGCGCTTACGAGAGCTTGTAGGAGC 525
 QY 595 GTGGTCAACCCCACTACCTGAGCAACGTGAGCGCGCGGCTTGTGCGCGCTGT 654
 Db 526 GTGGTCAACCCCACTACCTGAGCAACGTGAGCGCGCGGCTTGTGCGCGCTGT 585
 QY 655 GAGGCCAGCGGAACCGGCGCGGAAGTGGGAAGCTTCCGCAAGCTTTTACAGAGAC 714
 Db 586 GCGCCAGTGTGAACCGGCGCGGAAGTGGGAAGCTTCCGCAAGCTTTTACAGAGAC 645
 QY 715 CCCTGCTGGATGTGCATACAGCCTTTCAGACGTCGCAACCATCAGTTCTGCAGGAC 774
 Db 646 CCCTGCTGGATGTGCATACAGCCTTTCAGACGTCGCAACCATCAGTTCTGCAGGAC 705
 QY 775 CAG 777
 Db 706 CAG 708
 RESULT 7
 AAF57271
 ID AAF57271 standard; cDNA; 795 BP.
 XX AAF57271;
 AC 29-MAY-2001 (first entry)
 XX Mouse RetL5 polypeptide encoding cDNA.
 DE
 XX Ret ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; mouse;
 KM vulnerable; noctropic; anti-HIV; neuroprotective; antibacterial; ss;

CC The invention relates to mouse and human Ret ligand 5 (RetL5)
CC polypeptides. The RetL5 polypeptides can be expressed by standard
CC recombinant methodology. The RetL5 when bound to Ret, acts as a
CC dimerization or autophosphorylation activator. The polypeptides and their
CC antibodies are useful for stimulating growth of or limiting damage to,
CC Ret expressing tissue in a subject, for suppressing growth of a tumour
CC cell that expresses Ret, for modulating Ret signal transduction involving
CC a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion
CC proteins containing RetL5 and antibodies are useful for stimulating renal
CC tissue growth and/or survival, supporting renal function and minimizing
CC damage to renal tissue after various insults, particularly for treating
CC acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC injury and trauma. The compounds are also useful for treating conditions
CC such as neural degeneration where neural growth and regeneration are
CC desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC motor neuron disease, demyelinating disease, bacterial diseases, viral
CC diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC compounds are also useful for treating disorders due to damage to neural
CC tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC such as haemorrhage or emboli, and neural disorders such as mental
CC retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC palsy. The present sequence represents the mouse RetL5 cDNA sequence
CC predicted from DMS300 sequence by GENSCAN/GENE ALEX
XX
SQ Sequence 795 BP; 94 A; 271 C; 282 G; 148 T; 0 U; 0 Other;

OY		240	-----GGGCTGGAGGGGAACCCCGAGAGCTGGCGTGGCTCCCGTCGCGCGGTGGCCTTGAGC	294
Dd		166	CCCGAGGAGAGGCCGAGAACCCGAGGAGCTGCAGTCCCTCCCGTCGCGAGCCCTTGCGC	228
OY		295	CAGCTTTCTTCGCCCCCGAGGAGCTCCCGGCGCTCAACGCAACGAGCTGCTTTCTGCGATGCGAA	354
Dd		226	CGCTTCTTTCGCGGTGGGCTCCGAGGCTCAACGATGAGGCTGCTTTCTGCGGCTGGGAA	289
OY		355	GAGCCCGCGTGGCCGAGAGCGCGGCGCACATTCGCGCCCGCTGCGCTTTCCGAGC	414
Dd		286	GAGCTCCGCGAGCCCGAGCGCGGCGCACAGATTTCGCGCCGCTGCGCTTTCCGAGC	345
OY		415	CCCCAGTGGCGGCACTTCTCTGCTGAAAGCCCTTGGACGCGTGGAGCGAAGCGAGCGAG	474
Dd		346	CCGAGGTTGATGCGCGCTCTTTGCTTGAGACCCTTGGAGCGCTGGAGCGAGCGAGCGCTG	405
OY		475	TGCGGAGCCCGTCTCTTTCCTTCCAGAGGCTCATGCGCTCCCGGCGCGGCTCCCGAGC	534
Dd		406	TGCGGAGTGC-----GCTCATGCGCTCCCGGCGCGGCTCCCGAGC	447
OY		535	GAGCTGTCGAGAGAGGAGGAGCCCGCGGTGTCTGCGCGCTTACGAGGCTTTGTAAGCAC	594
Dd		448	CGCTGCGCCGAGAGAGGAGGAGCCCGGTTGTCTGCGCGCTTACGAGAGGCTCATAGGCAAC	507
OY		595	GTTGTCACCCCCCAAACCTAGACAACGTAAGCGCGCGCGGTGAGCCCTGGTGGCGGCTGT	654
Dd		508	GTTGTCACCCCCCAAACCTAGACAACGTAAGCGCGCGGTGAGCCCTGGTGGCGGCTGT	567
OY		655	GAGGCGAGCGGAAACCGGCGCGAGAAGTGCAGAGCTTCCGCAAGCTTTTATCAAGGAC	714
Dd		568	GCGGCGAGTGGAAAACCGGCGGCAAGATGCGAAGCTTCCGCAAGCTTTATCAAGGAC	627
OY		715	CCCTGCTGGATGTGCCATAACAGCTTTTGAACGCTCGCAACATCAGTTCTGACAGAC	774
Dd		628	CCCTGCTGGATGTGCCATAACAGCTTTTGAACGCTTTCAGCATCAGTTCTGACAGAC	687
OY		775	CAG 777	
Dd		688	CAG 690	
<hr/>				
RESULT 8				
AZ	ID	AZ28259	standard; cDNA; 1019 BP.	
XX	AAZ28259;			
XX	DT	05-JAN-2000	(first entry)	
XX	DE	Murine glial derived neurotrophic factor receptor-alpha-X cDNA.		
XX	XX			
KW	Glial derived neurotrophic factor-alpha-X; GFR-alpha-X; neural cell;			
KW	survival; function; nervous system; signaling; diagnosis; treatment;			
KW	neurological anaesthesia; sensory disorder; Dejerine-Roussy syndrome;			
KW	contralateral anaesthesia; eating disorder; obesity; motor disorder;			
KW	Parkinson's disease; amyotrophic lateral sclerosis; ALS;			
XX	cognitive disorder; Alzheimer's disease; ss.			
OS	Mus sp.			
PH	Key	Location/Qualifiers		
FT	CDS	1..1019		
FT		/+tag= a		
FT		/product= "Murine GFR-alpha-X protein"		
FT		/note= "No initiation or termination codons given in		
FT		specification"		
FT		/craml_except= (pos:601..603, aa:Xaa)		
FT		/note= "Xaa = unknown"		
FT		/craml_except= (pos:649..651, aa:Xaa)		
FT		/note= "Xaa = unknown"		
FT		/craml_except= (pos:1018..1019, aa:Xaa)		
FT		/note= "Xaa = unknown"		

XX
PN W09950298-A1.
XX
PD 07-OCT-1999.
XX
PF 25-MAR-1999; 99MO-US006631.
XX
PR 31-MAR-1998; 98US-0080070P.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Moore KJ;
XX
DR WPI; 1999-591276/50.
XX
P-PSDB; AAF42771.
XX
PT A nucleic acid molecule that encodes GDNF Family Receptor alpha-X
PT protein, methods of isolation and antibodies - useful for the detection
PT of homologues and identification of binding compounds.
XX
PS Claim 7, Fig 1; 100pp; English.
XX
XX This sequence represents murine glial derived neurotrophic factor
CC receptor-alpha-X (GFR-alpha-X) cDNA. GFR-alpha-X is a fourth member of
CC the glial derived neurotrophic (GFR-alpha) family of receptors. The cDNA
CC was identified in a positional cloning process in which the mouse
CC mahogany locus was being sequenced to identify genes involved in obesity.
CC The GFR-alpha-X protein binds to neurotrophic factors such as GDNF (glial
CC cell line-derived neurotrophic factor) and/or NTN (neurturin), and
CC mediates signalling within cells expressing the GFR-alpha-X protein. GFR-
CC alpha-X, like the other three members of the GFR-alpha family (GFR-alpha-
CC 1, -2, and -3), transmits a signal to the interior of a cell by
CC activation of the RBT protein tyrosine kinase signalling pathway.
CC Neurotrophic factors promote survival and function of neural cells of
CC both the central and peripheral nervous systems. Modulation of GFR-alpha-
CC X activity can result in modulation of the neurotrophic factor-initiated
CC cell function. Probes and/or primers derived from GFR-alpha-X cDNA, and
CC antibodies against the protein are used to detect the presence of GFR-
CC alpha-X nucleic acids or protein and can be used in the diagnosis and
CC treatment of a variety of neurological disorders, including sensory
CC disorders (e.g., Dejerine-Roussy syndrome, contralateral anaesthesia, and
CC certain eating disorders), motor disorders (e.g., Parkinson's disease,
CC amyotrophic lateral sclerosis), and cognitive disorders (e.g.,
CC Alzheimer's disease). In addition, compounds which bind to GFR-alpha-X
CC may be used to modulate the activity of the protein
XX
SQ Sequence 1019 BP; 148 A; 340 C; 343 G; 186 T; 0 U; 2 Other;

Query Match 48.3%; Score 487.2; DB 2; Length 1019;
Best Local Similarity 90.4%; Pred. No. 2.9e-94;
Matches 557; Conservative 0; Mismatches 48; Indels 11; Gaps 3;

QY 123 AGGGTCAGCGAGCTCACTAGAGGGGAATCGCTGCTGTAAGACGAGCGGTSCACAGC 182
DB 54 AGGCTCTGCGAGCTTTTACCGACGGGAATCGCTGCTGAGACCGGCCCAAGCGCTTACAGC 113
QY 183 AGACGACAGTGCAGCAGCAGCTGCGCTCCGAGTACGTGGCGCAATGCTTGGGCGGAGC--- 239
DB 114 AGACGACGCGGTGCCAGCAGCTGCGCTCGAGTACGTGGCAGAGTCCCTGGGCGGAGC 173
QY 240 -----GGGTCGGGGGAGCCCGGAGAGTGTGCTGCCCTCCGCTGGCGCGCTGCGC 293
DB 174 GCCCGGGGGGAGGCGCGGAGCCCGGGGGCTGCTGCCCTCCGCTGCCGCGACCCCTGCGC 233
QY 294 CCGCTTCTTGAGCCCGCGGAGCTCTCGGCGCTCAGCAGCGCGCTGCTTCTTGCGGATGCGA 353
DB 234 CCGCTTCTTGAGCCCGCGGAGCTCTCGGCGCTCAGCAGCGCGCTGCTTCTTGCGGATGCGA 293
QY 354 AGGCGCCGCGGTGCGCGAGCGCGCGCGCAGACATTCGCGCGCTCGCGCTTCTCGG 413
DB 294 AGGCTCGCGGTGCGCGAGCGCGCGCGCAGACATTCGCGCGCTCGCGCTTCTCGG 353
QY 414 CCCCAGCTGGCGCACCTTCTGCTGAGAGCCCTTGAGACCGCTGCGAGCGAGCCCGCG 473

DB 354 CCGGAGGTGTGTGCGCCCTCTTGCTTGGAGCCCTCGAGCGCTCGAGCGAGCCCGCT 413
QY 474 GTGCGGCGCCCGCTCTTGTGCTTCCAGAGGCTCATGCGCTCCGCGCCGCTCCGCGA 533
DB 414 GTGCGGCGCCCGCTCTTGTGCTTCCAGAGGCTCATGCGCTCCGCGCCGCTCCGCGA 473
QY 534 CCGCTGTCCGGAAGAGGGGGCGCGGTGTGCGCGCTTCCGAGGCTTGTAGGCGAC 593
DB 474 CCGCTGTCCGGAAGAGGGGGCGCGGTGTGCGCGCTTCCGAGGCTTGTAGGCGAC 533
QY 594 CGTGTACACCCCACTACTGAGACACGTAGCGCGCGCTTGGCGCCCTGTGCGGCTG 653
DB 534 CGTGTACACCCCACTACTGAGACACGTAGCGCGCGCTTGGCGCCCTGTGCGGCTG 593
QY 654 TGAAGCCA-GCGGAAACCGGCGCGAAGAGTGGAAAGCTTTCGCAAGCTTTTACAA-GG 711
DB 594 TGGGCGCANGTGGAAACCGGCGCGAAGATGGCAAGCTTTCGCAAGCTTTTACANAG 653
QY 712 AACCCCTGCTTGAGTG 727
DB 654 AACCCCTGCTTGAGTG 669

RESULT 9
AAF31061
ID AAF31061 standard; DNA; 2522 BP.
XX
XX AAF31061;
AC
XX
XX 06-APR-2001 (first entry)
DT
XX
XX Rat GFRalpha-4 gene.
DE
XX
XX Rat; GFRalpha-4; carcinoma; familial hirschsprung disease; pain;
KM glial cell-line derived neurotrophic factor; neurodegenerative disease;
KM GDNF family receptor alpha-4; Alzheimer's disease; Parkinson's disease;
KM motor neuron disease; peripheral neuropathy; spinal cord injury;
KM chromosome 3q36; ds.
OS
XX
XX Rattus rattus.
PN
XX W0200102557-A1.
PD 11-JAN-2001.
XX
XX 26-MAY-2000; 2000MO-EP004918.
PF
XX 29-JUN-1999; 99GB-00015200.
PR
XX (JANC) JANSSEN PHARM NV.
PA
XX Measure SLJ, Cjk M, Hofnagel EW;
PI WPI; 2001-138137/14.
XX
XX P-PSDB; AAB61636, AAB61637.
DR
XX
XX Glial cell-line derived neurotrophic factor family receptor alpha-4,
PT useful for preparing medicaments for treating neurodegenerative diseases
PT (e.g. Alzheimer's disease, Parkinson's disease) and carcinomas.
XX
XX
XX Claim 6; Page 71-72; 82pp; English.
PS
XX The present invention relates to rat Glial cell-line Derived Neurotrophic
CC Factor (GDNF) family receptor alpha-4 (GFRalpha-4; see AAB61636 and
CC AAB61637). The present sequence is the rat GFRalpha-4 gene. GFRalpha-4 is
CC useful in the preparation of a medicament for the treatment of
CC neurodegenerative diseases, Alzheimer's disease, Parkinson's disease,
CC motor neuron disease, peripheral neuropathy, spinal cord injury, familial
CC hirschprung disease, carcinomas, and diseases associated with GFRalpha-4
CC receptor dysfunction and in alleviating pain. The rat GFRalpha-4 gene is
CC localised on chromosome 3q36
XX

Sequence 2522 BP; 459 A; 707 C; 779 G; 577 T; 0 U; 0 Other;

Query Match 45.1%; Score 454.4; DB 4; Length 2522;

Best Local Similarity 82.3%; Pred. No. 3.1e-87; Indels 129; Gaps 2;

Matches 604; Conservative 0; Mismatches 1; Indels 129; Gaps 2;

123 AGGTCACGAGCTCCACTGAGGAGGATCGCTGCTGGAAGAGCCGAGCGCTGACAGC 182
 683 AGGTCACGAGCTCCACTGAGGAGGATCGCTGCTGGAAGAGCCGAGCGCTGACAGC 742
 183 AGACGAGAGTGTCCAGCAGCTGCTGCTGGAAGAGCCGAGCGCTGACAGC 242
 743 AGACGAGAGTGTCCAGCAGCTGCTGCTGGAAGAGCCGAGCGCTGACAGC 802
 243 CTGGGGGGGACCCGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
 803 CTGGGGGGGACCCGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 862
 303 CGCCGCGGGGCTCCGGGAGCTGACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
 863 CGCCGCGGGGCTCCGGGAGCTGACGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 922
 363 GTGCGCGAGCT 422
 923 GTGCGCGAGCT 982
 423 GCGCGCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 478
 983 GCGCGCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1042
 479 -----GGCCCGGCTCTTTG 493
 1043 CGTGGGGGCGGGCTGGGCGCGCTGACCGGCGCTCCGGGCGCGCGCGCGCGCGCGCTTTG 1102
 494 CTTTCACGAGCTTCATGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 553
 1103 CTTTCACGAGCTTCATGCGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1162
 554 GCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 587
 1163 GCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
 588 -----AGGAC 593
 1223 CGGGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1282
 594 CGTGTCACTCCCACTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 653
 1283 CGTGTCACTCCCACTGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1342
 654 TGAGCCAGCGGAAACCGGCGGAAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713
 1343 TGAGCCAGCGGAAACCGGCGGAAAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1402
 714 CCGCGCTTGGATG 727
 1403 CCGCGCTTGGATG 1416

RESULT 10

ABL51672 standard; cDNA, 810 BP.

ABL51672;

08-JUL-2002 (first entry)

Human GPI-anchored isoform a encoding cDNA SEQ ID NO:10.

GPRalpha4; glycosyl-phosphatidylinositol; GPI; GDNF; cytosolic; glycosyl-phosphatidylinositol-linked GDNF family alpha-receptor; glial cell line derived neurotrophic factor; osteopontin; tumour; neuroprotective; anticonvulsant; neoplasia; endocrine tumour;

medullary thyroid carcinoma; pheochromocytoma; parathyroid hyperplasia; neuronal disorder; aberrant axonal sprouting; gene; ss.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..810

FT product= "GPI-anchored isoform a"

MO200162795-A1.

30-AUG-2001.

14-NOV-2000; 2000WO-FI000994.

21-FEB-2000; 2000FI-0000394.

(LICE-) LICENTIA LTD.

Atkinson M, Saarna M, Poterisev D, Lindahl M, Timmusk T;

Rossi U;

WPI; 2001-596722/67.

P-PSDB; ABB09217.

New nucleic acid sequence for manufacturing polypeptides for treating

endocrine cancers comprises a cDNA encoding a splicing isoform of

mammalian growth factor receptor (GFR) alpha4.

Claim 4; Fig 21A; 143pp; English.

The present invention describes an isolated and purified cDNA sequence

encoding a splicing isoform of a mammalian growth factor receptor

(GFR) alpha4, or its fragments. GPRalpha4 sequences have cytosolic,

osteopontin, neuroprotective and anticonvulsant activities. GPRalpha4 is

a glycosyl-phosphatidylinositol (GPI)-linked glial cell line-derived

neurotrophic factor (GDNF) family alpha-receptor. A GPRalpha4 mediated

signalling in neurons or endocrine cells such as thyroid calcitonin-

producing C-cells, parathyroid gland cells, adrenal chromaffin cells, or

cells from the pituitary intermediate lobe. GPRalpha4 protein and

polynucleotide sequences can be used for manufacturing polypeptides

useful for diagnosing and/or treating tumours in parathyroid gland cells,

adrenal chromaffin cells, cells of pituitary intermediate lobe,

neoplasia, endocrine tumours, medullary thyroid carcinoma and

pheochromocytoma, parathyroid hyperplasia, neuronal disorders or for

preventing neuronal death or aberrant axonal sprouting. The present

invention encodes the human GPRalpha 4 protein, designated GPI-anchored

isoform a, from the present invention

Sequence 810 BP; 85 A; 314 C; 273 G; 138 T; 0 U; 0 Other;

Query Match 42.4%; Score 427.6; DB 4; Length 810;

Best Local Similarity 77.2%; Pred. No. 1.4e-81; Indels 9; Gaps 1;

Matches 536; Conservative 0; Mismatches 149; Indels 9; Gaps 1;

124 GAGTCAGGAGCTTCACCTGAGGAGGAGATGCTGCTGGAAGAGCGCGCTGACAGCA 183
 46 GAGTCAGGAGCTTCACCTGAGGAGGAGATGCTGCTGGAAGAGCGCGCTGACAGCG 105
 184 GACGAGAGTGTCCAGCAGCTGCTGCTGGAAGAGCGCGCTGACAGCGCGCGCGCGCG 243
 106 GACGAGAGTGTCCAGCAGCTGCTGCTGGAAGAGCGCGCTGACAGCGCGCGCGCGCG 161
 244 TGCGGGGAGCCCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
 162 -----TGCGAGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 216
 304 GCGCGCGGCTTCGAGCGCTGACGAGCGCTGCTTCTTGGAGTGGAGGCGCGCGCG 363
 217 GCGCGCGGCGCGCGCGCGCTACCGACGAGCTGCTTCTTGGAGTGGAGGCGCGCGCG 276

QY 364 TGGCGGAGCGCGGCCGACATTGCGCCCGCTGCGGCTTCCGCGCCCACTG 423
DB 277 TGGCGCCAGGCGTGGCCGACACCTTGCTGCTCCGCTTTCGGGGCCCGCC 336
QY 424 GCGGCACTTCTGCGCTGAAGCCCTTGAACCGGCGAGGAGGAGCGCGGTCGCGCC 483
DB 337 GCGCGGCTTCTGCTGCTGAAGCCCTTGAACCTTGAAGGAGGAGCGCGGTCGAGGCTT 396
QY 484 CGTCTCTTTCCTTTCAGGCTTCAATGCGCTCCGCGCGGCTTCCGCGAGCTGTCG 543
DB 397 CGGCTCTGCGCTTTCAGGCTTCAATGCGCTCCGCGCGGCTTCCGCGAGCTGTCG 456
QY 544 GAGGAGGCGCGCGCGGCTTTCAGGCTTCAATGCGCTCCGCGAGCTTTCAGGCTGTCAC 603
DB 457 CTGGAACGAGGCGCGCGGCTTTCAGGCTTCAATGCGCTCCGCGAGCTTTCAGGCTGTCAC 516
QY 604 CCGCACTTCTGCGCTGAAGGCGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 663
DB 517 CTTTACTTCTGCGCTGAAGGCGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 576
QY 664 GGAACCGGCGCGGAGGAGGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 723
DB 577 GGAACCGGCGGAGGAGGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 636
QY 724 GATGCTGCTTCAAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 783
DB 637 GATGCTGCTTCAAGGCTTTCAGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 696
QY 784 CCGTACGAGATGCTGCGGAGGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 817
DB 697 CCGTACGAGATGCTGCGGAGGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 730

RESULT 11

ID AAF57272 standard; cDNA; 849 BP.

AC AAF57272;

DT 29-MAY-2001 (first entry)

XX Human RetL5 polypeptide encoding cDNA.

XX RetL5 ligand 5; RetL5; autophosphorylation; tumour; renal; nephrotropic;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; human;
XX vulnerability; neurotropic; anti-HIV; neuroprotective; antibacterial; ss;
XX cerebroprotective; hemostatic; antiinflammatory; antiviral; neuroleptic.

OS Homo sapiens.

XX Location/Qualifiers

FT Key 1..849
FT CDS /*tag= a
FT /product= "RetL5"
FT sig_peptide 1..60
FT /*tag= b
FT mat_peptide 61..846
FT /*tag= c

XX NO200116169-A2.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-US024111.

XX 01-SEP-1999; 99US-0152024P.

XX (BIOJ) BIOGEN INC.

XX Worley D;

XX WPI, 2001-235091/24.

DR P-PSDB; AAB62105.

XX Novel Ret ligand polypeptide useful for suppressing growth of a tumor
PT cell that expresses Ret and for modulating Ret signal transduction
PT involving a cell expressing Ret polypeptide or Ret ligand polypeptide.
XX Claim 1, Fig 5; 76pp; English.

XX The invention relates to mouse and human Ret ligand 5 (RetL5)
CC polypeptides. The RetL5 polypeptides can be expressed by standard
CC recombinant methodology. The RetL5 when bound to Ret, acts as a
CC dimerization or autophosphorylation activator. The polypeptides and their
CC antibodies are useful for stimulating growth of or limiting damage to,
CC Ret expressing tissue in a subject, for suppressing growth of a tumor
CC cell that expresses Ret, for modulating Ret signal transduction involving
CC a cell expressing the Ret polypeptide. The RetL5 polypeptides, fusion
CC proteins containing RetL5 and antibodies are useful for stimulating renal
CC tissue growth and/or survival, supporting renal function and mimicking
CC damage to renal tissue after various insults, particularly for treating
CC acute renal failure, acute nephritis, chronic renal failure, nephrotic
CC syndrome, renal tubule defects, kidney transplants, toxic injury, hypoxic
CC injury and trauma. The compounds are also useful for treating conditions
CC such as neural degeneration where neural growth and regeneration are
CC desirable, e.g., Alzheimer's disease, Parkinson's disease, Huntington's
CC disease, Tourette's syndrome, amyotrophic lateral sclerosis, as well as
CC motor neuron disease, demyelinating disease, bacterial diseases, viral
CC diseases, and prion diseases including Creutzfeldt-Jakob disease. The
CC compounds are also useful for treating disorders due to damage to neural
CC tissue caused by neoplastic impingement, trauma or cerebrovascular events
CC such as hemorrhage or emboli, and neural disorders such as mental
CC retardation, autism, fetal alcohol syndrome, Down's syndrome and cerebral
CC palsy. The present sequence represents the human RetL5 cDNA sequence

XX Sequence 849 BP; 90 A; 330 C; 281 G; 148 T; 0 U; 0 Other;

Query Match 42.4%; Score 427.4; DB 4; Length 849;

Best Local Similarity 77.0%; Pred. No. 1.5e-81;

Matches 537; Conservative 0; Mismatches 151; Indels 9; Gaps 1;

QY 124 GGGTCAGCAGAGCTTCACCTAGGAGGATCGCTGAGAGAGCCGAGCGTGCACAGCA 183
DB 46 GGGTCAGCAGAGCTTCACCTAGGAGGATCGCTGAGAGAGCCGAGCGTGCACAGCA 105
QY 184 GAGCAGAGTGCAGAGCTGCGCTCCAGATGCTGCGCAATGCTTGGGCGGCGGCG 243
DB 106 GAGCAGAGTGCAGAGCTGCGCTCCAGATGCTGCGCAATGCTTGGGCGGCGGCGG 161
QY 244 TGGCGGAGAGCCGCGAGCTGCGCTCCGCTGCGCGGCGGCGGCGGCGGCGGCTTC 303
DB 162 ----TGGCGAGAGGAGCTGCGCTCCGCTGCGCGGCGGCGGCGGCGGCGGCTTC 216
QY 304 GCGCGGAGAGCTTCAGGCTTCAGCAGAGCTGCTTCTTGGGAGTGCAGAGGCGGCGG 363
DB 217 GCGCGGAGAGCTTCAGGCTTCAGCAGAGCTGCTTCTTGGGAGTGCAGAGGCGGCGG 276
QY 364 TGGCGGAGAGCTTCAGGCTTCAGCAGAGCTGCTTCTTGGGAGTGCAGAGGCGGCGG 423
DB 277 TGGCGGAGAGCTTCAGGCTTCAGCAGAGCTGCTTCTTGGGAGTGCAGAGGCGGCGG 336
QY 424 GCGGCACTTCTGCTGCTGAAGCCCTTGAACCGTGAAGGAGGCGGCGGCGGCGGCGG 483
DB 337 GCGGCGGCTTCTGCTGCTGAAGCCCTTGAACCTTGAAGGAGGCGGCGGCGGCGGCGG 396
QY 484 CGTCTCTTTCCTTTCAGGCTTCAATGCGCTCCGCGCGGCTTCCGCGAGCTGTCG 543
DB 397 CGGCTCTGCGCTTTCAGGCTTCAATGCGCTCCGCGCGGCTTCCGCGAGCTGTCG 456
QY 544 GAGGAGGCGCGCGGCTTTCAGGCTTCAATGCGCTCCGCGAGCTTTCAGGCTGTCAC 603
DB 457 CTGGAACGAGGCGCGGCTTTCAGGCTTCAATGCGCTCCGCGAGCTTTCAGGCTGTCAC 516
QY 604 CCGCACTTCTGCGCTGAAGGCGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 663
DB 517 CTTTACTTCTGCGCTGAAGGCGCGGCTTTCAGGCTTTCAGGCTTTCAGGCTGTCAC 576

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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:07:53 ; Search time 3963 Seconds

(without alignments)
9681.752 Million cell updates/sec

Title: US-10-019-337E-7

Perfect score: 1008
Sequence: 1 ctgctaagcttaagcaga.....aactccttcgctcctcagtc 1008Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_hnc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	395.2	39.2	950	5	BUS14417 AGENCOURT
2	391.4	38.8	796	5	BUS14417 AGENCOURT
3	387.6	38.5	679	6	BY733470 BY733470
4	385.6	38.3	805	5	BUS59540 AGENCOURT
5	382.6	38.0	1084	3	AKO90192 Mus muscu
6	378.4	37.5	704	7	CR835860 4060515 B
7	258.8	25.7	792	1	AU035938
8	255.2	25.3	955	5	BUS14417 AGENCOURT
9	217	21.5	499	5	BUS14417 AGENCOURT
10	206	20.4	454	2	BF565913
11	202	20.0	497	1	AA823200
12	170	16.9	788	7	CO884025
13	148	14.7	735	5	BK101753
14	143.8	14.3	633	6	CB097266
15	139.6	13.8	822	7	CNS3269 UI-M-HUO-
16	135.8	13.5	699	4	BM724059 UI-E-E01-
17	132.2	13.1	581	4	BUS39556 452275 MA
18	132	13.1	537	2	AM632211
19	131.6	13.1	806	7	CR028763
20	131	13.0	845	6	CA487292
21	130.4	12.9	538	1	BM363287
22	129.8	12.9	205	4	AI465648
23	129.2	12.8	4556	3	AK076171
24	128.8	12.8	4191	3	BC040251

25	125	12.4	395	6	CB76051	CB76051 AMGNNUC:S
26	123.6	12.3	602	5	CA887225	CA887225 B0135E01-
27	123	12.2	904	5	BU956631	BU956631 AGENCOURT
28	122.2	12.1	662	4	B1196287	B1196287 602755202
29	121.2	12.0	419	8	A2715993	A2715993 RCT-24-8
30	120.8	12.0	942	5	B0857306	B0857306 AGENCOURT
31	119	11.8	742	4	B1917824	B1917824 603183943
32	117.8	11.7	4383	3	BC011532	BC011532 Mus muscu
33	117.8	11.7	4618	3	BC044783	BC044783 Mus muscu
34	112.4	11.2	446	1	AA387098	AA387098 vc18b07.r
35	111.4	11.1	631	1	AA518362	AA518362 v110d02.r
36	111	11.0	969	5	BU955785	BU955785 AGENCOURT
37	110	10.9	823	7	CN232349	CN232349 WLB049A05
38	106.4	10.6	772	6	CB526842	CB526842 UI-M-FY0-
39	105.8	10.5	669	2	CD775377	CD775377 UI-M-A00-
40	104	10.3	500	2	AM372397	AM372397 RC6-BT033
41	103.6	10.3	541	2	AM372400	AM372400 RC6-BT033
42	98.2	9.7	890	5	BX709568	BX709568 BX709568
43	97	9.6	873	1	AL552892	AL552892 AL552892
44	95.6	9.5	562	5	BX857143	BX857143 BX857143
45	95	9.4	183	2	BE655865	BE655865 UI-M-BG0-

ALIGNMENTS

RESULT 1
BUS14417
LOCUS
DEFINITION AGENCOURT10119656 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6511038 5', mRNA sequence.
BUS14417 GI:22821943

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC http://mgc.ncl.nih.gov/
1 (bases 1 to 950)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LLM41080 row: 0 column: 07
High quality sequence stop: 573.
Location/Qualifiers

FEATURES

1..950
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/db_xref="taxon:10090"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_134"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; site 2: NotI;
cloned unidirectionally. Primer: Oligo dt. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC library."

ORIGIN

Query Match 39.2%; Score 395.2; DB 5; Length 950;
Best Local Similarity 82.4%; Pred. NO. 3.8e-81;
Matches 496; Conservative 0; Mismatches 88; Indels 18; Gaps 3;
415 CCCAGGTGGCGCACCTCTCTGAGCCCTTGACCGCTGCGAGCGAAGCGCGG 474

Db	52	CCGCGCTGCGCGGATGCGTGCCTGGCGGGGCGGAGCTTGGGCGCGCTCAACCCGCGCTCCGGGCGCG	111
Qy	475	TGCGGCGCCCGGTCTCTTTGGCTTTCAGAGCCTTCATGCGTCCCGCGGCCGCGCTCCGCGAC	534
Db	112	CGAGAGGCCCGCTCTCTTGGCTTTCAGAGCCTTCATGCGTCCCGCGGCCGCGCTCCGCGAC	171
Qy	535	GCGTGTCCGAGAGAGAGGGGAGCCGCGAGTGTCTGCGCGCTTACGCAAGCCTTGTATGAGCAC	594
Db	172	CGCTGCCCGAGAGAGGGGGGCGCGGTGTGTCTGCGCGCTTACGCAAGCCTTATGAGCAC	231
Qy	595	GTGCTCAACCCCACTACTGTGACAAGTGAAGCGCGCGCTTGGCGCCTGTGTGGGCTGT	654
Db	232	GTGTGTACCCCACTACTGTGACAAGTGAAGCGCGCGCTTGGCGCCTGTGTGGGCTGT	291
Qy	655	GAGCCAGACGAGAACCCGCGCGAAGAGTGCAGAGCCTTCCGCAAGCTTTTACAGAGAAC	714
Db	292	GCGGCGAGTGAACCCGCGCGAGAGATGCGAAGCTTTCGCAAGCTTTTACAGAGAAC	351
Qy	715	CCCTGCTTGAATGCTGCATACAAAGCCTTTGACAGCTCGCAACATCAATTCTGCAGGAC	774
Db	352	CCCTGCTTGAATGCTGCATACAAAGCCTTTGACAGCTCGCAACATCAATTCTGCAGGAC	411
Qy	775	CAGTGAAACCCCTACAGAAATGCTGGGCGAGGCGAAAGTGGAGGCGTGAAGGCTGAGAA	834
Db	412	CAG-----ACTGCTGGGTGCTGTTTTCCGCGGGCAAGGCGCAAGTGGCTGAGAA	461
Qy	835	GAGATGAGCAGAAACGATCCCGCTTTTGT-----CCCAAGTGTCTCGATGTCA	887
Db	462	GAGCTGGAGGAGAAACAGTCTTTGTTGTCTTAACGCCCAAGGTGTCTCGCTGTATG	521
Qy	888	TACTACATCGCCCTGGCTCTCCAGGCGCGTCTCTATTAGAAAGGTGAACCATGACAACA	947
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Db	582	CAGCTGAATGCAATGTCTCCGATGAATGCTGCTCACTGAAGTGAATCTCCCTTGCCTCAGG	641
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[illegible]

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/clone="IMAGE:6591416"
/_lab_host="DH10B (TI-phage-resistant)"
/_clone_id="N1H_MGC_144"
/note="Organ: Brain; Vector: pDNR-LIB; Site_1: SfiI
(ggcatcattggcgc); Site_2: SfiI (ggcgcgcgcgcgc); cDNA made
by oligo-dT priming and directionally cloned; 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGATTCAGCAGAGATGGCCATTCAGCGCCGG-3' and
5'-ATCTTAGAGCCCGAGGCGCCGCAATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in N1H MGC 143)
library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a N1H_MGC Library."

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Query Match	38.8% ; Score 391.4 ; DB 5 ; Length 796 ;
Best Local Similarity	81.1% ; Pred. No. 2.9e-80 ;
Matches 488 ;	Conservative 0 ; Mismatches 81 ; Indels 18 ; Gaps 3 ;
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Qy	490 TTTTGCCTTCCAGGCGCTCATGGCTCTCCGCGCCCGGCTCCCGCAACGGTGTCCGAGAG 549
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Qy	550 GGGGGCCCGGGGTGTCTCGCGGCTTACGAGGCGCTTGAAGCACGGTGTACACCCCAAC 609
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Qy	610 TACCTGCAACAACGTGACGCGCGCGTTCGCGCTGTGCGGCTGTGAGGCGACGCAAC 669
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Qy	670 CGGCGCAAGAGTGCAGAACCTTCCGCAAGCTTTTACAAGAAACCCCTGCTTGATGT 729
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Qy	730 GCCATAACAGCTTTGACAGTGCACACCATCAATCAATTTCTGACAGGACAGTGAACCCCTAC 789
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Qy	790 CAGATCTGGGCGAGCGCAAGGTGAGAGGCTGATGTGCTGAGAGAGATGAGAGCA 849
Db	355 TGCTGGGTGCTGTTTCCCGCGGCGAGGACAGATGCTGAGAGAGCTGAGAGCA 414
Qy	850 ACGGTCCCGCTTTTGT-----CCCAAGTGTCTCGATGTCATATCTACCTCCCTGG 902
Db	415 ACAGTCTCTGTTTGTCTTACGCGCCAAAGGTGCTCTGAGTGTATGCACTACCTCCCTGG 474
Qy	903 CTCTCCAGGCGCTCTCTCTAATTAGAGAGGTGAACATGAGACACAACAGCTACTGCAATG 962
Db	475 CTCTCCAGGCGCTCTCTCTGATTAGAGACATGAACCCGTGAGAGACACAGCTACTGCAATG 534
Qy	963 TCTCTGAGTTA-TGCTCAGTGAACCTGAACCTCCCTGAGCCCTCAGATC 1008
Db	535 TCTCCGATGACTGCTCACTGAGCTGAACCTCCCTGAGCCCTCAGATC 581

RESULT 3
BY733470

LOCUS
BY733470

DEFINITION
BY733470 RIKEN full-length enriched, 16 days neonate male
dienecephalon Mus musculus cDNA clone G630015H18 5', mRNA sequence.

ACCESSION
BY733470

VERSION
BY733470.1 GI:27146597

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 679)

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Otsu, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schirra, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Brusic, V., Chochua, C., Corbett, L. E., Cousins, S., Datta, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kanao, H., Kawasawa, Y., Keizer, R. M., King, B. L., Komagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Matsuda, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sadelain, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Mura, M., Nakamura, N., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, M., Muramatsu, M., and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation

JOURNAL

Nature 420, 563-573 (2002)

MEDLINE

22354683

COMMENT

Contact: Yoshihide Hayashizaki; Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashizaki, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Mura, M., Nakamura, N., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Saeki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watanabe, M., Muramatsu, M., and Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

1. 679 Location/Qualifiers
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/mol_type="mRNA"
/accession="CS7BL/6J"
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ORIGIN

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Best Local Similarity 82.0%; Pred. No. 2.2e-79;
Matches 489; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

415 CCCGAGTGGGCGCCACTTCTGCTGTAAGCCCTGAGACCGCTGAGAGCGGCGCG 474
10 CCGCTGCTGCGGCGCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 69
475 TGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 534
70 CGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 129
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130 CGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 189
595 GTGGTCAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 654
190 GTGGTCAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 249
655 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 714
250 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 309
715 CCGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774
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775 CAGTGAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 834
370 CAG-----ACTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 419
835 GAGTGAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 887
420 GAGTGAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 479
888 TACGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 947
480 CACTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
948 CAGTGAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 1002
540 CAGTGAACCCCACTAAGTGAACAGTGAACAGTGAACAGTGAACAGTGAACAGTGA 595

RESULT 4

BUS59540 805 bp mRNA linear EST 16-SEP-2002

LOCUS

BUS59540 805 bp mRNA linear EST 16-SEP-2002

DEFINITION

AGENCOURT 10336959 NIH MGC_144 Mus musculus cDNA clone

ACCESSION

BUS59540 805 bp mRNA linear EST 16-SEP-2002

VERSION

BUS59540 805 bp mRNA linear EST 16-SEP-2002

KEYWORDS

BUS59540.1 GI:22909836

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 805) NIH-MGC http://mgi.nci.nih.gov/

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)

JOURNAL

Contact: Robert Strauberg, Ph.D.

COMMENT

Contact: Robert Strauberg, Ph.D.

Email: cgsabos-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

FEATURES

Location/Qualifiers

ORIGIN

Query Match	38.3%;	Score 385.6;	DB 5;	Length 805;
Best Local Similarity	86.6%;	Pred. No. 6.4e-79;		
Matches 466; Conservative	0;	Mismatches 54;	Indels 18;	Gaps 3;

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Db	1	GGGCGCGTCTCTTGGCTTTCAGGCGCTATGGCTCCCGGCGCGGCTCCCGCAACGGT	60
Qy	539	GTCCGGAGAGAGGGGGGCCCGCGGTGTCTGGCGGCTTAAGCAAGGCTTTGTAAGGACCGTGG	598
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Qy	599	TCACCCCAATACCTGTGACAAACGAGACGCGCGGCTTGCGGCTCTGGAGCGGCTGTGAG	658
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Qy	779	GGAACCCCTTACAGAAATGCTGGGCGAGCGCAAGTGAAGAGCCTGAATGGCTTAGAAGAGA	838
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Qy	952	TGACTGCATGTCTCTGATTA-TGCTCACTGAATGAACATCTCCTTGCCCTCAAGTC	1008
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ACCESSION	DEFINITION	LOCUS
AK090192	Mus musculus 16 days neonate male diencephalon cDNA, RIKEN full-length enriched library, clone:G650015H18 product:glial cell line-derived neurotrophic factor family receptor alpha 4, full insert sequence.	AK090192
AK090192	AK090192.1 GI:26355273	1084 bp mRNA
VERSION	HTC, CAP trapper.	linear
KEYWORDS	Mus musculus (house mouse)	HTC 03-APR-2004
SOURCE	Mus musculus	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE	2	
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Normalization and subraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE	20499374	
PUBMED	11042159	
REFERENCE	3	
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	

TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshitake Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploratory Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp)
COMMENT URI: <http://genome.gsc.riken.jp/>; Tel:81-45-503-9222, Fax:81-45-503-9216
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>.

FEATURES

SOURCE

location/Qualifiers

1..1084

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/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="PANTOM DB:G63001SH18"

/db_xref="taxon:10090"

/clone="G63001SH18"

/sex="male"

/tissue_type="dienecephalon"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="16 days neonate"

102..515

/note="Unamed protein product, glial cell line derived

neurotrophic factor family receptor alpha 4

(MGI:MGI:1341873, GB|NM_020014, evidence: BLASTV, 99%,

match=474)

putative"

/codon_start=1

/protein_id="BAC41129.1"

/db_xref="GI:2635274"

/translation="MRSRARLPRLPGGGALSLRLRPHRHGHPOLPGQRARAC

ALVAVPVERGAKNKSASLSLQGTAMVPLVPLACSHQFQRTLLAVNSGGGT

SGARRAGRNPCVLTPIKYSMLYALRALAQALL"

1066..1071

/note="putative"

1084

/note="putative"

ORIGIN

Query Match 38.0%; Score 382.6; DB 3; Length 1084;

Best Local Similarity 82.1%; Pred. No. 3.3e-78;

Matches 495; Conservative 0; Mismatches 89; Indels 19; Gaps 4;

415 CCCAGCTGGGCGCACTTCTGCTGAGCGCTTGAAGCGGCTGGAGCGAAGCGCGG 474

10 CCGCTGTGCGGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 69

475 TGGCGGCGGCGGCTCTTCTTCCAGGCTTCATGCGCTCCCGCGCGCGCGCGAC 534

70 CGCAGGCGGCGGCTCTTCTTCCAGGCTTCATGCGCTCCCGCGCGCGCGCGAC 129

535 GCGTGTCCGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 594

130 CGTGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 189

595 GTGTGACCGCCCACTACCTGAGCAAGTGAAGCGGCGGCGGCGGCGGCGGCGGCGG 653

190 GTGTGACCGCCCACTACCTGAGCAAGTGAAGCGGCGGCGGCGGCGGCGGCGGCGG 249

654 TGAAGCGGCGGAGAACCGGCGGCGGAGAGTGAAGCGGCGGCGGCGGCGGCGGCGG 713

250 TGGCGGCGGAGAACCGGCGGCGGAGAGTGAAGCGGCGGCGGCGGCGGCGGCGG 309

714 CCGCTGTGAGTGTGCTATACAGCCTTGAAGCTTGAAGCGGCGGCGGCGGCGGCGG 773

310 CCGCTGTGAGTGTGCTATACAGCCTTGAAGCGGCGGCGGCGGCGGCGGCGGCGG 369

774 CCAGTGAACCCCTACCAAGATGCTGGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 833

370 CCAG-----ACGCTGGGCTGCTTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 419

834 AGAGATGAGGCGAGAAACGCTCCCGTTTGT-----CCCAAGTGTCTTCGATGCC 886

420 AGAGCTGAGGCGAGAAACGCTCTTTTGTCTTGAAGCGGCGGCGGCGGCGGCGGCGG 479

QY 887 ATACTACTGGCTGGCTGCTCTTCAGAGCGGCTGCTTAATTAGAGAGTGAACATGACAC 946

DB 480 GCACCTAGCTGCTGGCTGCTCTTCAGAGCGGCTGCTTAATTAGAGAGTGAACATGACAC 539

QY 947 ACAGCTAGCTGCAATGCTCTGATTA-TGCTCACTGAAGTGAAGTCCCTTGGCTCAG 1005

DB 540 ACAGCTAGCTGCAATGCTCTGATTA-TGCTCACTGAAGTGAAGTCCCTTGGCTCAG 599

QY 1006 GTC 1008

DB 600 GTC 602

RESULT 6

LOCUS CK835860 704 bp mRNA linear EST 04-MAR-2004

DEFINITION 4060515 BARC 8BOV Bos taurus cDNA clone 8BOV_14117 5', mRNA

sequence. CK835860

ACCESSION CK835860.1 GI:45067634

VERSION EST.

KEYWORDS Bos taurus (cow)

SOURCE Bos taurus

ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 704)

AUTHORS Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. and

Matukumalli,L.K.

TITLE Construction and Analysis of a cDNA Library Generated From

Intestinal Muscle and Epithelial Tissues of Holstein Cattle

Unpublished (2004)

COMMENT Contact: Richard G. Baumann

NRRI Bovine Functional Genomics Lab

BLDG 162; BARC-EAST, Beltsville, MD 20705, USA

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@nrri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt ' ' -trim fasta. Vector identified

by cross match using options -mismatch 12 -mismatch 12

Plate: 14 row: I column: 17

Seq primer: CTTATTGAGTGAACCTATGAAC

High quality sequence stop: 704.

location/Qualifiers

1..704

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Holstein"

/db_xref="taxon:9913"

/clone="8BOV_14117"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stage="Lactating, Neonatal"

/lab_host="DH10B TONa"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: PCWVSPORT6.1; Site: 1:

NotI; Site 2: EcoRI; Normalized cow cDNA intestinal

library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources, 4 lactating intestinal, 1

neonatal intestinal 4/5 Lactating, Proximal Duodenum, 1

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal

ORIGIN

Query Match 37.5%; Score 378.4; DB 7; Length 704;

Best Local Similarity 74.8%; Pred. No. 3e-77;

Matches 491; Conservative 0; Mismatches 156; Indels 9; Gaps 1;

164 CAGCGGAGCGGTGACAGACGAGAGTGGCGAGCTGGCGTCCGATGAGTGGCGC 223

DB 1 CGGCGGAGCGGTGACAGACGAGAGTGGCGAGCTGGCGTCCGATGAGTGGCGC 60

QY	224	AATGCTCGAGGCGCGGAGCGAGCTGAGCGAGGAAACCGGAGAGCTGGTGCCTCCCGCTGCGGC	283
Db	61	AGTCTGTTGGGTGCTGTC-----CGCGCGGGGGGTGCCCCCGCGCTGCGGC	111
QY	284	GTGCTTCGCGCGCTTCTTTCGCGCGGAGCTCTCGAGCGCTCAGCGAGCGCTGCTTCTT	343
Db	112	GGCGCTTGCGCCACTTCTTCGCTCCGCGGAGCGCGCTTACCCACAGCACTGCTCTTCT	171
QY	344	GGCGATGGGAAGGCGCGCGTGGGCGCAGAGCGCGGCGCACAACATGCGCGCGCGCTGCG	403
Db	172	GCCCTTGCGCGGCGCGCGCGTGGCGAGAGCGCGCGCAGCACTTCTGTCCTCTGCG	231
QY	404	CGTTCCTCGGCGCCCAAGCTGAGCGCACTTCTCTGCTTGAAGCCTTGGACCGCTGCGAGC	463
Db	232	CTTTCTCAGGGGCTTGCGCGCGGCGCACTTCTCTGCTCGGAGCCTTGAATGCTTGAGC	291
QY	464	GAGCGCGCGGTGCGCGCGCTCTTCTTTCCTTCAGGCTCATGCGCTCCGCGCGCG	523
Db	292	ACAGCCCGAGTCTGAGGCGCGCGCTCTTCAGTCTCTCGCGCGACAGCA	351
QY	524	GCTCCCGCGAGCGGCTGTCGCGAGGAGGAGGCGCGCGCGTGTCTGCGGCGCTTACGAGGCG	583
Db	352	GCAACCTTGACGGCTGCTCCGAGACAGGCGCCCACTGCTTGCGGCGCTTACGCGGCGC	411
QY	584	TTGTAGGCAACCGTGTGCAACCCCACTACCTGGAACAAGTGAAGCGCGCGCTTGCGGCT	643
Db	412	TGCGGAGCAGACCATGACGCGCCCACTACGTAAGTGAACAAGCAAGCGCGCGTGAAGCCT	471
QY	644	GGTGCGGCTGTGAGAGCCGAGCGGAAACCGCGCGCAAGATGGGAAGCTTTCGCAAGCTT	703
Db	472	GTGTCGACTGAGAGCAAGCAAGCGGAAATCGCGTGAAGATGGGAAGTCTTCGAGGAGCTCT	531
QY	704	TTAACAGGAACCCCTGCTTGGATGGTGTCATACAAAGCTTTGACAGCTCGCAACCATGAG	763
Db	532	TTACGAGGAACCGCTGCTTGAACAGTGCACATACAGACTTTGACGATGGTGGCGCCCA	591
QY	764	TTCTGCAAGAACCAATGGAACCCCTAACAGAAATGCTGGGACGCAAGGTGAGGCG	819
Db	592	TCTACGTAACCACTGGACTCCACCAAGAGCCTGAGACAGATGCTCTGCAAGGTC	647
RESULT 7			
AU035938		792 bp	mRNA linear EST 12-JUL-2000
LOCUS			
DEFINITION			AU035938 Sugano mouse brain mncb Mus musculus cDNA clone MNcb-1073,
ACCESSION			mRNA sequence.
VERSION			AU035938
KEYWORDS			AU035938.1 GI:3718946
SOURCE			EST.
ORGANISM			Mus musculus (house mouse)
REFERENCE			Mus musculus
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 792)
TITLE			Saeki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K., Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
JOURNAL			Construction of mouse full length-enriched cDNA libraries
COMMENT			Unpublished (1998) Contact: Kazuyuki Hashimoto Division of Genetic Resources National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan Email: khashi@nih.go.jp
FEATURES			POLYA=No.
source			Location/Qualifiers
			1..792
			/organism="Mus musculus"
			/mol_type="mRNA"
			/strain="C57BL"
			/db_xref="taxon:10090"
			/clone="MNcb-1073"
			/sex="female"

		/dev stage="adult"	
		/lab host="TOP10"	
		/clone_1lb="Sugano mouse brain mmbch"	
		/note="Torgan; Drain; Vector: pME185-FL3; 1st strand cDNA	
		was primed with an oligo(dt) primer	
		ATGAGCGCTTTTATTATTTTTTTT); double-stranded cDNA was	
		ligated to a DraIII adaptor [GTGGCCACTACGG], digested and	
		cloned into distinct DraIII sites of the pME185-FL3. XhoI	
		sites just outside the DraIII sites can be used to isolate	
		the cDNA insert. Size selection was performed to exclude	
		fragments <1.5 kb. Library was constructed by Sugano et	
		al.(University of Tokyo, Institute of Medical Science).	
		Custom primer used for sequencing: 5' end primer	
		[CTMGTCCTTAAGCTGGG], 3' end primer	
		[CGACCTGCAGCTCGACACA]"	
ORIGIN			
Query Match	25.7%; Score 258.8; DB 1; Length 792;		
Best Local Similarity	80.9%; Pred. No. 1.9e-49;		
Matches 338; Conservative	0; Mismatches 27; Indels 53; Gaps 1;		
QY	363 GTGCGCCGAGCGCGCGGCCAGACATTGCGCGCCTGCGCGCTTCTCCGCGCCCCCACT	422	
Dd	1 GTGCGCCGAGCGCGCGGCCAGACTTTTCGCGCGCCTGCGCGCTTCTCCGCGCGCGGTT	60	
QY	423 GGCGCCACCTTCCGCGCTGAAGCCCTTGAAACCGCTGCGAAGCAAGCCCGCGTGC----	478	
Dd	61 GGTGCGCGCTTCTGCTTGGCTGAAGCCCTTGAAAGCGTGAAGCGCACCGCGCTGTGCTGG	120	
QY	479 -----GGCCCGCTCTC	489	
Dd	121 CGTGCAGCGGCGGCGGCTGGGCGCGCTCACCGCGCTCGGCGCGCGCGCGCGCGCTTC	180	
QY	490 TTGCTCTTCCAAGCGCTCATGCGCTCCCGCGCGCGCGCTCCCGCAAGCGCTGTGCGAAGAG	549	
Dd	181 CTGCTCTTCCAAGCGCTCATGCGCTCCCGCGCGCGCGCTCCCGCAAGCGCTGTGCGAAGAG	240	
QY	550 GGGGGCCCCGGGTCTGCGCGCGCTTAGCGAGCGCTTTGAGCACCGTGTACACCCCAC	609	
Dd	241 GGGGGCCCCGGGTGTGCGCGCTTAGCGAGCGCTTACGAGCACCGTGTACACCCCAC	300	
QY	610 TACCTGACACAGCGAGCGCGCGCTTGCGCGCTGTGCGGCTGTGAGAGCCAGCGCAAC	669	
Dd	301 TACCTGACACAGCGAGCGCGCGCTTGCGCGCTGTGCGGCTGTGAGAGCCAGCGCAAC	360	
QY	670 CCGCGCGAAGAGTGCAGAGCTTCCGCAAGCTTTTACAAAGAACCCCTGCTTGATG	727	
Dd	361 CCGCGCGAAGAGTGCAGAGCTTCCGCAAGCTTTTACAAAGAACCCCTGCTTGATG	418	
RESULT 8			
Bu604828	955 bp mRNA linear EST 20-SEP-2002		
LOCUS	AGENCOUR10055539 NIH MGC144 Mus musculus cDNA clone		
DEFINITION	IMAGE:6535992 5', mRNA sequence.		
ACCESSION	Bu604828		
VERSION	Bu604828.1 GI:23256587		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 955)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strauberg, Ph.D.		
	Email: cgabs-rc@mail.nih.gov		
	Tissue Procurement: Dr. Michael Brownstein		
	cDNA Library Preparation: Michael Brownstein Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		

QY	842	AGGAGAAAGGTRCCCGTTTGT-----CCCAAGTGTCTCGATGTCCATCTAC	894
Db	172	AGGAGAAAGTCTCTGTGTTTGTCTTAACGCCCAAGGTGTCTGTATGCACTCAC	231
QY	895	TGCCCTGGCTCTCCAGAGCCCTGCTCTAATTAGGAAGTGAACCATGACAACAGCTGA	954
Db	232	TGCCCTGGCTCTCCAGAGCCCTGCTCTAATTAGGAACATGAACCGTGAACACAGCTGA	291
QY	955	CTGCACGTCTCTTGATTA-TGCTCACTGAACCTGAACTCCCTTGGCCCTCAGTTC	1008
Db	292	CTGCACGTCTCCCGATGACGTCTCACTGAGCTGAACCTCCCTTGGCCCTCAGGTC	346
RESULT 10			
LOCUS	BF565913		
DEFINITION	BF565913	454 bp	mRNA
	UI-R-BOL-ajr-c-09-0-UI.r1	linear	EST 12-DEC-2000
	UI-R-BOL-ajr-c-09-0-UI 5',		mRNA sequence.

ACCESSION BF565913
VERSION BF565913.1 GI:11675643
KEYWORDS
SOURCE
ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 454)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LMNL (info@image.liml.gov). IMAGE ID= 1798704
Seq primer: M13 Forward.

FEATURES
source

1..454
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-ajf-c-09-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="UI-R-B01"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B01) is a subcloned library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"

ORIGIN

Query Match 20.4%; Score 206; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 3.3e-37; Indels 0; Gaps 0;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 803 AGGCCAAGTGGAGGCTGAGTGGCTGAGAGAGATGAGGACGAAACGGTCCCGTTT 862
DB 5 AGGCCAAGTGGAGGCTGAGTGGCTGAGAGAGATGAGGACGAAACGGTCCCGTTT 64
QY 863 TGTGCCAAGGTCTCTGATGTCCATATCTCACTGCCCTGGCTCTCCAGGCCCTGCTTAA 922
DB 65 TGTGCCAAGGTCTCTGATGTCCATATCTCACTGCCCTGGCTCTCCAGGCCCTGCTTAA 124
QY 923 TTGAGAGGTGAACCATGAGCAACACAGCTGACCTGACATGCTCTGATTATGCTCACTG 982
DB 125 TTGAGAGGTGAACCATGAGCAACACAGCTGACCTGACATGCTCTGATTATGCTCACTG 184
QY 983 AACTGAACCTCCCTTGGCCTCAGGTC 1008
DB 185 AACTGAACCTCCCTTGGCCTCAGGTC 210

RESULT 11
AA823200
5

LOCUS AA823200 497 bp mRNA linear EST 17-FEB-1998
DEFINITION t41h08.r1 Soares mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1246431 5', mRNA sequence.
ACCESSION AA823200
VERSION AA823200.1 GI:2893068
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 497)

REFERENCE
AUTHORS
Matta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Watson, R. and
Waterson, R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maira M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LMNL; contact the
IMAGE Consortium (info@image.liml.gov) for further information.
MGI:660119

Seq primer: -28mJ rev2 ET from Anersham
High quality sequence stop: 443.
Location/Qualifiers
1..497
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1246431"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_1lb="Soares mammary_gland_NbMMG"
/note="Organ: mammary gland; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGGCGCCGGAATGTTTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

ORIGIN

Query Match 20.0%; Score 202; DB 1; Length 497;
Best Local Similarity 81.8%; Pred. No. 2.8e-36;
Matches 288; Conservative 0; Mismatches 45; Indels 19; Gaps 4;
QY 665 GAAACGGGCGGAGAGTGGAGGCTTCCGAGCTTTTACAGAAACCCCTGCTGG 724
DB 3 GAAACGGGCGGAGAGTGGAGGCTTCCGAGCTTTTACAGAAACCCCTGCTGG 61
QY 725 ATGTGTCATACAGGCTTTGACAGTCCGCAACCATCACTTTGCGAGGACGATGAAAC 784
DB 62 ATGTGTCATACAGGCTTTGACAGTCCGCAACCATCACTTTGCGAGGACG----- 114
QY 785 CCTACAGATGTGGGAGGCGCAAGTGGAGGCTTGAAGTGGCTGAGAGATGAGG 844
DB 115 ---ACTGCTGGGTGCTTTTCCCGCGGAGGACGATGCTGAGAGAGCTGAGG 171
QY 845 CAGAAACGCTCCCGTTTGT-----CCCAAGTGTCTCGATGCATATCACTGCG 897
|||||

Db 172 CAGAAACAGCTCTTTGTTGCTTAACGCCCAAGGTGCTGCTGTATGACTACCTAGC 231
 Qy 898 CCGTGCCTCCAGGCCCCGCTCTAATTAAGAGTGAACCATGAGCAACAGCTGACTG 957
 Db 232 CTGAGCTCTCCAGGCGCTGCTGTATTAAGAACATGAACCGGTGACGACAGCTGACTG 291
 Qy 958 CCATGCTCTGAGTTA-TGCTCACTGAACGTAAATCCCTTGCCTCAGCTC 1008
 Db 292 CCAATGCTCCGAGTACGTCTCACTGAGCTAACTCCCTTGCCTCAGCTC 343

RESULT 12
 CO884025 788 bp mRNA linear EST 01-SEP-2004
 LOCUS BOVGEN13250 normal cattle brain Bos taurus cDNA clone
 DEFINITION RZDP105612017Q 5', mRNA sequence.
 ACCESSION CO884025
 VERSION CO884025.1 GI:51813969
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 788)
 Hennig,S., Janitz,M., Herwig,R. and Williams,J.
 Generation, annotation, evolutionary analysis and database integration of 14969 cattle EST clusters
 Unpublished (2004)
 JOURNAL Contact: Hennig S
 LABORATORY 123, dept. Lebrach
 Max-Planck-Institut fuer Molekulare Genetik
 Inmestr.65-73, D-14195 Berlin, Germany
 Tel: +49 30 8413 1612
 Fax: +49 30 8413 1380
 Email: hennig@molgen.mpg.de
 The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (http://www.rzpd.de).
 PCR Primers
 FORWARD: 5' CCCGAGGCTTTACACTTATGCTCCGCTG 3' (M13RSP) 5'-seq
 BACKWARD: 5' GCTATTACGCCAGCTGCGAAGGAGGATGTG 3' (M13FSP) 3'-seq
 Seq primer: 5'-CCGTCGCGAATTCCCGCGT-3' (M13RSP).
 Location/Qualifiers
 1..788
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="RZDP105612017Q"
 /sex="female"
 /tissue_type="brain tissue"
 /dev_stage="adult brain"
 /clone_lib="normal cattle brain"
 /note="Organ: brain; Vector: pSport1; Site 1: NotI; Site 2: SalI; Random primed and directionally cloned in pSport1 vector using NotI (5'-pGACTACTTCTAGATCGGAGCGCGGCC (7)15-3' and SalI 5'-TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"
 TCGACCCACGCGTCCG-3' adapters (Gibco BRL)"

ORIGIN
 Query Match 16.9%; Score 170; DB 7; Length 788;
 Best Local Similarity 64.6%; Pred. No. 8.1e-29;
 Matches 283; Conservative 0; Mismatches 130; Indels 25; Gaps 1;

Qy 509 GCGCTCCGCGCCGCTCCGCGACGCTGTCCGAGAGAGGGGCGCGGTGTCTGC 568
 Db 10 GCGGACCAACAGCAAGCCCTGACGGCTCTCCGAGACCAAGGCCCCGAGCTGCCGC 69
 Qy 569 GCGGCTACGACGAGGCTTTAGGACACCGTGTACACCCCACTACTGACAAAGTGAAG 628

Db 70 GCGCTACGCGGCGCTGTGGGACACAGCATACAGCCCACTAGTGGACAAACCAAGCG 129
 Qy 629 CGCGCTTGGGCGCCCTGTGTGGGCTGTGAGGCGCACCGGAAACCGGCGGAGAGTCCGAG 688
 Db 130 CGCGCGTGGAGGCCCTGTGTGGGCTGTGAGGCGCACCGGAAACCGGCGGAGAGTCCGAG 189
 Qy 689 CCTTCGCGCAAGCTTTTACAGAGAAACCGCTGTGTGAGTGTGTCATCAAGCTTTTGACA 748
 Db 190 TCTTCGCGGAGGCTTTTACAGAGAAACCGCTGTGTGAGTGTGTCATCAAGCTTTTGAGC 249
 Qy 749 GCTGCAACCATCATGTTCTGAGAGACCAAGTGAACCCCTACAGAAATGCTGGGAGGCCA 808
 Db 250 GTGGGTGGCCCGCCCAATCTCAGTACCAACATGAGCTCCACACAGACCTTGAGCAGATC 309
 Qy 809 AGGTGAGGCGCTGAGTGGCTGTGAGAAAGATGAGGAGCAAAACGCTCCCTTTGTGCC 868
 Db 310 TCTCTGAGGTGTCTACAGAGATGCGCCCTGGAGG----- 345
 Qy 869 AAGGTGCTCGATGTCATCTACAGTGCCTGTGCTCCAGGCGCTGTCTAATTAAGA 928
 Db 346 -AGAGCTCCGCTCTCAGTGTCTTGTGTGAGCTCTCCAGTCCCTGTGTGAGCTTGA 404
 Qy 929 AGGTGAACCATGAGCAAC 946
 Db 405 CAGCAGACCTTGACCAAC 422

RESULT 13
 BX101753 735 bp mRNA linear EST 06-FEB-2003
 LOCUS BX101753
 DEFINITION IMAGp99801021 ; IMAGE:124377, mRNA sequence.
 ACCESSION BX101753
 VERSION BX101753.1 GI:27831358
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 735)
 Ebert,L., Heil,O., Hennig,S., Neubert,P., Parsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
 Human Unigeneset - RZPD3
 Unpublished (2003)
 JOURNAL Contact: Ina Rolfs
 LABORATORY RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGp99801021.
 RZPDLIB: I.M.A.G.E. cDNA clone collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 M13r, Primer sequence: TTTTACACAGAAACAGCTATGAC.
 Location/Qualifiers
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 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS"
 /note="Organ: Liver and Spleen; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: PYX-5.
 Location/Qualifiers

FEATURES
source

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/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_HU0"
/note="Organ: Eye; Vector: pyx-asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-asc vector. The library tag sequence located between the Not I site and the polyA tail is AATAATGCG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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ORIGIN

Query Match 13.8%; Score 139.6; DB 7; Length 822;
 Best Local Similarity 55.6%; Pred. No. 9.4e-22;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2005, 01:31:13 ; Search time 2729 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	299.6	29.7	995	US-10-152-661-604	Sequence 604, App
3	216.4	21.5	207433	US-10-277-216-5	Sequence 5, Appli
4	216.4	21.5	207433	US-10-126-022-5	Sequence 5, Appli
5	150.4	14.9	1392	US-09-388-316-2	Sequence 2, Appli
6	150.4	14.9	1392	US-10-357-822-2	Sequence 2, Appli
7	150.4	14.9	1490	US-10-673-007-10	Sequence 10, Appli
8	150.4	14.9	1995	US-09-388-316-15	Sequence 15, Appli
9	150.4	14.9	1995	US-10-357-822-15	Sequence 15, Appli
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ALIGNMENTS

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; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 604
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Mouse
US-09-866-050A-604

Query Match 29.7%; Score 299.6; DB 10; Length 995;
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RESULT 2

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1 Sequence 604, Application US/10155261
2 Publication NO. US20030022835A1
3 GENERAL INFORMATION:
4 APPLICANT: Watson, James D.
5 APPLICANT: Strachan, Lorna
6 APPLICANT: Steeman, Matthew
7 APPLICANT: Onrust, Rene
8 APPLICANT: Mursion, James G.
9 APPLICANT: Kumble, Krishanand D.
10 TITLE OF INVENTION: Compositions Isolated From Skin Cells
11 TITLE OF INVENTION: and Methods for Their Use
12 FILE REFERENCE: 11000.1011c5
13 CURRENT APPLICATION NUMBER: US/10/152,661
14 PCT NO. 03/022,835
15 PCT FILING DATE: 2002-05-20
16 PRIORITY CLAIM: 09/866,050
17 PRIORITY CLAIM: 2001-05-24
18 PRIORITY CLAIM: 60/221,232
19 PRIORITY CLAIM: 2000-07-25
20 PRIORITY CLAIM: 60/206,650
21 PRIORITY CLAIM: 2000-05-24
22 PRIORITY CLAIM: 09/312,283
23 PRIORITY CLAIM: 1999-05-14
24 PRIORITY CLAIM: PCT/NZ99/00051
25 PRIORITY CLAIM: 1999-04-29
26 PRIORITY CLAIM: 09/188,930
27 PRIORITY CLAIM: 1998-11-09
28 PRIORITY CLAIM: 09/069,726
29 PRIORITY CLAIM: 1998-04-29
30 NUMBER OF SEQ ID NOS: 725
31 SOFTWARE: FastSeq for Windows Version 4.0
32 SEQ ID NO 604
33 LENGTH: 995
34 TYPE: DNA
35 ORGANISM: Mouse
36 US-10-152-661-604

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Query Match	29.7%;	Score 299.6;	DB 14;	Length 995;
Best Local Similarity	77.8%;	Pred. No. 5.6e-78;		
Matches 420; Conservative	0;	Mismatches 49;	Indels 71;	Gaps 2;

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RESULT 3

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US-10-277-216-5/c
; Sequence 5, Application US/10277216
; Publication No. US20040002470A1
; GENERAL INFORMATION:
; APPLICANT: KEITH, TIM
; TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES
; FILE REFERENCE: 2976-4051
; CURRENT APPLICATION NUMBER: US/10/277,216
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 10/126,022
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 09/834,597
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/548,797
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 207433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-277-216-5

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Query Match	21.5%	Score 216.4;	DB 17;	Length 207433;
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Db 367 CTGACGTCCCTGGCTCTCCAGAGCCCTGCTCTAATTAGAGAGGAGGAGCAACACA 426
QY 950 GCTGACGTCCATGTCTGTGATTA-TGCTCACTGAACTGAAACTCCCTGCTCAGATC 1008
Db 427 GCTGACGTCCATGTCTGTGATTA-TGCTCACTGAACTGAAACTCCCTGCTCAGATC 486

RESULT 2
US-08-957-063-2
; Sequence 2, Application US/08957063
; Patent No. 6025157
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957, 063
; FILING DATE: 24-Oct-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/871
; FILING DATE: 9-Jun-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 913
; FILING DATE: 18-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1086P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-957-063-2

Query Match 14.9%; Score 150.4; DB 3; Length 1392;
Best Local Similarity 56.0%; Pred. No. 7e-27;
Matches 355; Conservative 0; Mismatches 261; Indels 18; Gaps 3;
QY 123 AGGGTCAGCGAGCCCACTGAGGGGGAATCGCTGCTGGAAGCAGCCGAGGCGTGCACAGC 182
Db 450 AGACCCCGGTGTCAAGCCGCAAGACACACATTGCTGATGCTGCCAAGGCTGCAACT 509
QY 183 AGACGACAGTGCAGCAGAGCTGCCTCCGAGTACGTGCGCAATGCCCTGGGCGGCGG 242
Db 510 GAATGACATGCAAGAAAGCTGGCTCTCTCTCATCTCCATCTGCAACGCGGATCTC 569
QY 243 CTGGCGGGGAGCCCGGAGCTGCGTGGCTCCCGCTGCCCGCGGCTGCGGCGCTTCTT 302
Db 570 -----GCCACCGAGCGCTGCAACCGCCGCAAGTGCACAAAGGCGCTGCGCCAGTTCTT 623

QY 303 CGCCCGCGGACCTCCGCGCTCAGCAGCGCTGCTCTTCTGCGGATGGAAGCCCGCC 362
Db 624 CGACCGGCGTGGCCAGAGATACACCTACCGCANGTCTTCTGCTCCTGCGAAGACAGGAC 683
QY 363 GTGCGCCGAGCGCCCGGCGCCAGACATTCGCGCCGCTGCGGCTTCTCCGCCCCAGCT 422
Db 684 GTGCGCTGAGCGCCCGCGGCAACCATCTGCGCCAGCTG-----CTCTATGAGGACAA 737
QY 423 GCGCGCACCTTCCTGCTGAGCGCTTGGAGCCGCTGCGAGGAGCGCGGTCGCGGC 482
Db 738 GAGAAAGCCCACTGCTTGAACCTGCGTGTGCGGTGCGGATGACCACTGTGTGCTG 797
QY 483 CGCTCTCTTGTGCTTCCAGCCTCAATGCGCTCCCGGCGCCGCTCCCGGAGCGCTGTC 542
Db 798 CGCGGTGGCGGACTTCATGCAATGTGTGAGCGCTCTACAGAGGTGATCAGCAGCTGCC 857
QY 543 GAGAGAGGGGGGCGCGCGGTGTGTGCGCCCTACAGAGGCTTGTAGGACCGTGTAC 602
Db 858 TGGGGAACAATTAACAGGCGTGTCTGGGCTTTATGTGACATGATGGGTTTGACATGAC 917
QY 603 CCCCACTACCTGAGCAACGTGAGCGCGCGCTGCG-----CCCTGTGCGGCTGTGA 656
Db 918 ACTTAATATGTGAGCTCCAGCCCACTGCGATCGTGTGCTCCCTGTGATGACGTGTG 977
QY 657 GGCACGCGGAAACCGCGCGGAAAGTGCAGAGCTTCCGCAAGCTTTTACAGAAACC 716
Db 978 TGGCAGCGGGAACATGAGAGAGAGTGTGAGAACTTCTCAGGAGCTTCAACGAGAACCC 1037
QY 717 CTGCTGATGTGTGCTATCAAGCTTTTGACAGC 750
Db 1038 ATGCTTCGGAAGCGCATCCAGGCTTTGGCAAC 1071

RESULT 3
US-09-487-685-2
; Sequence 2, Application US/09487685
; Patent No. 6342348
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/487, 685
; FILING DATE: 19-Jan-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/957, 063
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 913
; FILING DATE: 18-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1086P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1392 base pairs